GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 12, 2003, 18:06:22 ; Search time 21 Seconds
(without alignments)
638.692 Million cell updates/sec

Title: US-09-891-138A-2
Perfect score: 1650
Sequence: 1 MAQNLSCENWLATEAILNKY.....REMLISKFRQYFKSLTSFRT 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1226.5	74.3	334	2	US-08-559-524A-2	Sequence 2, Appli
2	1226.5	74.3	334	3	US-08-749-707-2	Sequence 2, Appli
3	474	28.7	373	2	US-08-559-524A-4	Sequence 4, Appli
4	474	28.7	373	3	US-08-749-707-4	Sequence 4, Appli
5	473.5	28.7	362	3	US-08-513-974B-374	Sequence 374, App
6	372	22.5	374	4	US-09-102-710B-3	Sequence 3, Appli
7	370.5	22.5	373	3	US-08-513-974B-373	Sequence 373, App
8	353	21.4	355	1	US-08-153-848-28	Sequence 28, Appl
9	353	21.4	355	1	US-08-153-848-32	Sequence 32, Appl
10	353	21.4	355	3	US-09-299-843A-28	Sequence 28, Appl
11	353	21.4	355	3	US-09-299-843A-32	Sequence 32, Appl

12	353	21.4	355	4	US-09-088-337B-28	Sequence 28, Appl
13	353	21.4	355	4	US-09-088-337B-32	Sequence 32, Appl
14	353	21.4	355	4	US-09-170-496D-130	Sequence 130, App
15	353	21.4	355	4	US-09-170-496D-232	Sequence 232, App
16	353	21.4	355	5	PCT-US93-11153-28	Sequence 28, Appl
17	353	21.4	355	5	PCT-US93-11153-32	Sequence 32, Appl
18	338	20.5	328	3	US-08-513-974B-39	Sequence 39, Appl
19	338	20.5	328	3	US-08-513-974B-371	Sequence 371, App
20	338	20.5	328	4	US-09-461-436B-39	Sequence 39, Appl
21	336.5	20.4	360	3	US-08-875-573-20	Sequence 20, Appl
22	336.5	20.4	360	3	US-09-232-878-2	Sequence 2, Appli
23	336.5	20.4	360	3	US-09-045-583-55	Sequence 55, Appl
24	336.5	20.4	360	4	US-09-534-185-55	Sequence 55, Appl
25	336.5	20.4	360	4	US-08-939-107-34	Sequence 34, Appl
26	335.5	20.3	375	1	US-08-442-134A-2	Sequence 2, Appli
27	335.5	20.3	375	1	US-08-444-581B-2	Sequence 2, Appli
28	335.5	20.3	375	1	US-08-446-088A-2	Sequence 2, Appli
29	335.5	20.3	375	2	US-08-559-524A-3	Sequence 3, Appli
30	335.5	20.3	375	3	US-08-749-707-3	Sequence 3, Appli
31	329	19.9	355	3	US-09-045-583-53	Sequence 53, Appl
32	329	19.9	355	4	US-09-534-185-53	Sequence 53, Appl
33	328	19.9	355	1	US-08-012-988A-2	Sequence 2, Appli
34	328	19.9	355	1	US-08-450-393A-5	Sequence 5, Appli
35	328	19.9	355	3	US-08-446-669-5	Sequence 5, Appli
36	328	19.9	355	4	US-09-239-938-1	Sequence 1, Appli
37	328	19.9	355	4	US-09-886-319A-14	Sequence 14, Appl
38	328	19.9	355	5	PCT-US95-00476-5	Sequence 5, Appli
39	326.5	19.8	360	4	US-08-833-752-10	Sequence 10, Appl
40	325.5	19.7	346	4	US-09-585-876-2	Sequence 2, Appli
41	325	19.7	302	2	US-08-467-948A-30	Sequence 30, Appl
42	325	19.7	302	3	US-08-467-947A-30	Sequence 30, Appl
43	325	19.7	328	3	US-08-513-974B-56	Sequence 56, Appl
44	325	19.7	328	3	US-08-513-974B-380	Sequence 380, App
45	325	19.7	328	4	US-09-461-436B-56	Sequence 56, Appl

ALIGNMENTS

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RESULT 1
US-08-559-524A-2
; Sequence 2, Application US/08559524A
; Patent No. 5871963
;  GENERAL INFORMATION:
;    APPLICANT:  Conley, Pamela B.
;    APPLICANT:  Jantzen, Hans-Michael
;    TITLE OF INVENTION:  NOVEL PURINERGIC RECEPTOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN, LEWIS & BOCKIUS LLP
;      STREET:  1800 M Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036-5869
;    CCMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/559,524A
;       FILING DATE:  15-NOV-1995
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Adler, Reid G.
;       REGISTRATION NUMBER:  30,988
;       REFERENCE/DOCKET NUMBER:  044481-5010-00-US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-467-7000
;       TELEFAX:  202-467-7176
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  334 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-559-524A-2

  Query Match             74.3%;  Score 1226.5;  DB 2;  Length 334;
  Best Local Similarity   71.5%;  Pred. No. 4e-93;
  Matches  226;  Conservative   42;  Mismatches   47;  Indels    1;  Gaps    1;

Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
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Db          5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:|||| ||||||||||||| ||||||||||||:||||::
Db         65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

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Db        125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
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Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
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Db        305 MLMNQLRHNFKSLTSF 320


RESULT 2
US-08-749-707-2
; Sequence 2, Application US/08749707
; Patent No. 6063582
;  GENERAL INFORMATION:
;    APPLICANT:  Conley, Pamela B.
```

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;    APPLICANT:  Jantzen, Hans-Michael
;    TITLE OF INVENTION:  NOVEL PURINERGIC RECEPTOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN, LEWIS & BOCKIUS LLP
;      STREET:  1800 M Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036-5869
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/749,707
;      FILING DATE:  15-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Adler, Reid G.
;      REGISTRATION NUMBER:  30,988
;      REFERENCE/DOCKET NUMBER:  044481-5010-01-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-467-7000
;      TELEFAX:  202-467-7176
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  334 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-749-707-2

  Query Match             74.3%;  Score 1226.5;  DB 3;  Length 334;
  Best Local Similarity   71.5%;  Pred. No. 4e-93;
  Matches  226;  Conservative   42;  Mismatches   47;  Indels    1;  Gaps    1;

Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              || | :|:|||| || | ||||| || |||: |:||| ||:||:| :|||||||:||||
Db          5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:|||| |||||||||||||| ||||||||||||:||||::
Db         65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||| |||||||||||||:| |||||:||:|  || |  : |: | |:||||:| :|
Db        125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
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Db        185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 244

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:|||||| || |  |||  | | | :|| | |||| |||:||||:|||:|:
Db        245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRALGFLNSVINPVFYFLLGDHFRD 304
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RESULT 3
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; Sequence 4, Application US/08559524A
; Patent No. 5871963
;  GENERAL INFORMATION:
;    APPLICANT:  Conley, Pamela B.
;    APPLICANT:  Jantzen, Hans-Michael
;    TITLE OF INVENTION:  NOVEL PURINERGIC RECEPTOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN, LEWIS & BOCKIUS LLP
;      STREET:  1800 M Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036-5869
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/559,524A
;      FILING DATE:  15-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Adler, Reid G.
;      REGISTRATION NUMBER:  30,988
;      REFERENCE/DOCKET NUMBER:  044481-5010-00-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-467-7000
;      TELEFAX:  202-467-7176
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  373 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-559-524A-4

  Query Match             28.7%;  Score 474;  DB 2;  Length 373;
  Best Local Similarity   36.6%;  Pred. No. 1.9e-31;
  Matches  105;  Conservative   58;  Mismatches  116;  Indels    8;  Gaps    6;

Qy          20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
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Db          52 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 111

Qy          80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
                |     :|| :|   |:: | ||| ||||| ||  ||  : || :     ||: |: |
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Db        112 FNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAVYI 171

Qy        139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
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Db        172 SVLVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSMCTTVAMFCVPLV 231

Qy        198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
              ::   | :|  | :    :   ||  |   ||:: : :|:: : |:|:|: : : :||
Db        232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 288

Qy        257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
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Db        289 DFQTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335


RESULT 4
US-08-749-707-4
; Sequence 4, Application US/08749707
; Patent No. 6063582
;  GENERAL INFORMATION:
;    APPLICANT:  Conley, Pamela B.
;    APPLICANT:  Jantzen, Hans-Michael
;    TITLE OF INVENTION:  NOVEL PURINERGIC RECEPTOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN, LEWIS & BOCKIUS LLP
;      STREET:  1800 M Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036-5869
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/749,707
;      FILING DATE:  15-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Adler, Reid G.
;      REGISTRATION NUMBER:  30,988
;      REFERENCE/DOCKET NUMBER:  044481-5010-01-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-467-7000
;      TELEFAX:  202-467-7176
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  373 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-749-707-4

  Query Match             28.7%;  Score 474;  DB 3;  Length 373;
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  Best Local Similarity   36.6%;  Pred. No. 1.9e-31;
  Matches  105;  Conservative   58;  Mismatches  116;  Indels    8;  Gaps    6;

Qy         20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
              ||| | | : || | |||   :: ::| || |:  :||:|||:::|| :: ||| ||  |
Db         52 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 111

Qy         80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
               |     :|| :|   |:: | ||| |||||| ||  ||  : || :     ||: |: |
Db        112 FNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAVYI 171

Qy        139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
              |: || :| : : |:| :  : : | :   | |  |         |||:| |:  | :||
Db        172 SVLVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSMCTTVAMFCVPLV 231

Qy        198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
              ::   | :|  | :    :   ||  |   ||:: : :|:: : |:|:|: : : :||
Db        232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 288

Qy        257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
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Db        289 DFQTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335
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RESULT 5
US-08-513-974B-374
; Sequence 374, Application US/08513974B
; Patent No. 6114139
;  GENERAL INFORMATION:
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Hosoya, Masaki
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Ohtaki, Tetsuya
;    APPLICANT:  Fukusumi, Shoji
;    APPLICANT:  Ohgi, Kazuhiro
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
;    TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;    NUMBER OF SEQUENCES:  380
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/513,974B
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP95/01599
;      FILING DATE:  10-AUG-1995
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;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-093989
;       FILING DATE:  19-AUG-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-057186
;       FILING DATE:  16-MAR-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-007177
;       FILING DATE:  20-JAN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-326611
;       FILING DATE:  28-DEC-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-270017
;       FILING DATE:  02-NOV-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-236357
;       FILING DATE:  30-SEP-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-236356
;       FILING DATE:  30-SEP-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189274
;       FILING DATE:  11-AUG-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189273
;       FILING DATE:  11-AUG-1945
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189272
;       FILING DATE:  11-AUG-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Resnick, David S.
;       REGISTRATION NUMBER:  34,235
;       REFERENCE/DOCKET NUMBER:  45753
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-523-3400
;       TELEFAX:  617-523-6440
;   INFORMATION FOR SEQ ID NO:  374:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  362 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-513-974B-374

  Query Match             28.7%;  Score 473.5;  DB 3;  Length 362;
  Best Local Similarity   35.9%;  Pred. No. 2e-31;
  Matches  110;  Conservative   57;  Mismatches  122;  Indels   17;  Gaps    8;

Qy         10 WLA----TEAILNK-----YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              | |    |:  | |     |||   | : || | |||   :: ::| |: |:  :||:||
Db         22 WAAGNATTKCSLTKTGFQFYYLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMFN 81

Qy         61 LSISDFAFLCTLPILIKSYANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLL 119
              |:::|| :: ||| ||  | |     :|||:|   |:: | ||| |||||| ||: ||
Db         82 LALADFLYVLTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYTG 141
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Qy         120 MKYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFIN-SVPKEEGSNCIDYASSGNPE 178
               : :| :     ||: |: :|  |||||   : |:| :    | : :   | |  :
Db         142 VVHPLKSLGRLKKKNAVYVSSLVWALVVAVIAPILFYSGIGVRRNKTITCYDTTADEYLR 201

Qy         179 HNLIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIF 237
                 :||:| |:  | ||  |:   |  :|  |  :    :   ||  |   ||:: : :|
Db         202 SYFVYSMCTTVFMFCIPFIVILGCYGLIVKALIYKDLDNS---PLRRKSTYLVIIVLTVF 258

Qy         238 SILFTPYHIMRNLRIASRLD-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGD 295
               :: : |:|:|: | : :|||   || |     : : | :|| || ||| ::|| ||| ||
Db         259 AVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNSCVDPILYFLAGD 318

Qy         296 HYREML 301
                :|  |
Db         319 TFRRRL 324
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RESULT 6
US-09-102-710B-3
; Sequence 3, Application US/09102710B
; Patent No. 6479630
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: A NOVEL HUMAN PURINERGIC P2U RECEPTOR
; FILE REFERENCE: PF-0038-1 DIV
; CURRENT APPLICATION NUMBER: US/09/102,710B
; CURRENT FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PERL Program
; SEQ ID NO 3
;   LENGTH: 374
;   TYPE: PRT
;   ORGANISM: Rattus norvegius
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: RNU09402
US-09-102-710B-3

  Query Match   22.5%; Score 372; DB 4; Length 374;
  Best Local Similarity   33.8%; Pred. No. 4.3e-23;
  Matches   96; Conservative   49; Mismatches 125; Indels   14; Gaps   7;

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Qy          19 KY-YLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIK 77
               ||  |   | :  : ||  ||  :: :|  :| ||:|  |:|:|::||  :  :||:|:
Db          32 KYVLLPVSYGVVCVLGLCLNVVALYIFLCRLKTWNASTTYMFHLAVSDSLYAASLPLLVY 91

Qy          78 SYA-NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAI 136
                ||  |   :  |||   |:: :|||| |||||| ||: | | :  |          :|
Db          92 YYAQGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRSLGVLRPLHSLRWGHARYAR 151

Qy         137 LISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPL 196
                ::  || ||     |:| |: :  :     | | :      | : ||  :  | | :|
Db         152 RVAAVVWVLVLACQTPVLYFVTTSVRGTRITCHDTSDRELFSHFVAYSSVMLGLLFAVPF 211
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Qy         197 SVMCFFYYKMVVFLKRRSQQQA---TALPLDKPQ--RLVVLAVVIFSILFTPYHIMRNLR 251
               |::   |    | : ||  : |   | ||  | :  | : | : :|:: | |:|: | |
Db         212 SIILVCY----VLMARRLLKPAYGTTGLPRAKRKSVRTIALVLAVFALCFLPFHVTRTLY 267

Qy         252 IASRLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMG 294
                : |  |    | |  ||   | :|||||  || ::|: |||  |
Db         268 YSFR--SLDLSCHTLNAINMAYKITRPLASANSCLDPVLYFLAG 309


RESULT 7
US-08-513-974B-373
; Sequence 373, Application US/08513974B
; Patent No. 6114139
;  GENERAL INFORMATION:
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Hosoya, Masaki
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Ohtaki, Tetsuya
;    APPLICANT:  Fukusumi, Shoji
;    APPLICANT:  Ohgi, Kazuhiro
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
;    TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;    NUMBER OF SEQUENCES:  380
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/513,974B
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP95/01599
;      FILING DATE:  10-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-093989
;      FILING DATE:  19-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-057186
;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-007177
;      FILING DATE:  20-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-326611
;      FILING DATE:  28-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-270017
;      FILING DATE:  02-NOV-1994
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;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-236357
;       FILING DATE:  30-SEP-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-236356
;       FILING DATE:  30-SEP-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189274
;       FILING DATE:  11-AUG-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189273
;       FILING DATE:  11-AUG-1945
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189272
;       FILING DATE:  11-AUG-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Resnick, David S.
;       REGISTRATION NUMBER:  34,235
;       REFERENCE/DOCKET NUMBER:  45753
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-523-3400
;       TELEFAX:  617-523-6440
;   INFORMATION FOR SEQ ID NO:  373:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  373 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-513-974B-373

  Query Match             22.5%;  Score 370.5;  DB 3;  Length 373;
  Best Local Similarity   33.5%;  Pred. No. 5.7e-23;
  Matches   94;  Conservative   50;  Mismatches  130;  Indels    7;  Gaps    5;

Qy         19 KY-YLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIK 77
              ||  |    | :  : ||  ||  :: :|  :| ||:|  |:|:|::||  :  :||:|:
Db         32 KYVLLPVSYGVVCVLGLCLNVVALYIFLCRLKIWNASTTYMFHLAVSDSLYAASLPLLVY 91

Qy         78 SYA-NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAI 136
               ||  |   :  |||   |:: :|||| |||||| ||: | | :  |       :  :|
Db         92 YYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLHSLRWGRARYAR 151

Qy        137 LISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPL 196
              ::  || ||     |:| |: :  :     | | ::     | : ||  :  | | :|
Db        152 RVAAVVWVLVLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSSVMLGLLFAVPF 211

Qy        197 SVMCFFYYKMVVFLKRRSQQQATALPLDKPQ--RLVVLAVVIFSILFTPYHIMRNLRIAS 254
              ||:   |  |   | : :      ||  | :  | : | : :|:: | |:|: | |  :
Db        212 SVILVCYVLMARRLLKPAYGTTGGLPRAKRKSVRTIALVLAVFALCFLPFHVTRTLYYSF 271

Qy        255 RLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMG 294
              |  |    | |  ||   | :|||||  || ::|: ||| |
Db        272 R--SLDLSCHTLNAINMAYKITRPLASANSCLDPVLYFLAG 310


RESULT 8
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```
US-08-153-848-28
; Sequence 28, Application US/08153848
; Patent No. 5759804
;  GENERAL INFORMATION:
;    APPLICANT:  Godiska, Ronald
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Schweikart, Vicki L.
;    TITLE OF INVENTION:  No. 5759804el Seven Transmembrane Receptors
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/153,848
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/977,452
;      FILING DATE:  17-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5759804and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31794
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-153-848-28

  Query Match             21.4%;  Score 353;  DB 1;  Length 355;
  Best Local Similarity   28.1%;  Pred. No. 1.5e-21;
  Matches   84;  Conservative   66;  Mismatches  133;  Indels   16;  Gaps    6;

Qy          16 ILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPIL 75
               :    :|| ||:: |  ||:||: |||      |  : :::|| ||::||  |: |||
Db          28 VFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSDLLFVATLPFW 87

Qy          76 IKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA 135
                    |:|| : : :|          : || |:| ||:|||| :         :  :
Db          88 THYLINEKGLH-NAMCKFTTAFFFIGFFGSIFFITVISIDRYLAIVLAANSMNNRTVQHG 146
```

```
Qy        136 ILISLAVWALVTLEVLPMLTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLI 194
              : ||| |||   |   |   |     |:: : |: ||         :: ::    ||||:
Db        147 VTISLGVWAAAILVAAPQFMF----TKQKENECLGDYPEVLQEIWPVLRNVETNFLGFLL 202

Qy        195 PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIA 253
              || :| : |::::      :: ::| |:      :|::| |::| : :|||::|  |
Db        203 PLLIMSYCYFRIIQTLFSCKNHKKAKAI------KLILLVVIVFFLFWTPYNVMIFLETL 256

Qy        254 SRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
                | :|    :| ::   ::|  :|| :  :||: |   |: :|  |   :  | | |
Db        257 KLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYL---YHLYGKCL 312
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```
RESULT 9
US-08-153-848-32
; Sequence 32, Application US/08153848
; Patent No. 5759804
;  GENERAL INFORMATION:
;    APPLICANT:  Godiska, Ronald
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Schweikart, Vicki L.
;    TITLE OF INVENTION:  No. 5759804el Seven Transmembrane Receptors
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/153,848
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/977,452
;      FILING DATE:  17-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5759804and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31794
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
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US-08-153-848-32

Query Match 21.4%; Score 353; DB 1; Length 355;
Best Local Similarity 28.1%; Pred. No. 1.5e-21;
Matches 84; Conservative 66; Mismatches 133; Indels 16; Gaps 6;

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Qy          16 ILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPIL 75
               :    :|| ||:: |  ||:||: |||      |  : :::|| ||::||  |: |||
Db          28 VFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSDLLFVATLPFW 87

Qy          76 IKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA 135
                    |:|| : : :|           : || |:| ||:|||| :          :  :
Db          88 THYLINEKGLH-NAMCKFTTAFFFIGFFGSIFFITVISIDRYLAIVLAANSMNNRTVQHG 146

Qy         136 ILISLAVWALVTLEVLPMLTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLI 194
               : ||| |||   |   |   |     |:: : |: ||         :: ::    ||||:
Db         147 VTISLGVWAAAILVAAPQFMF----TKQKENECLGDYPEVLQEIWPVLRNVETNFLGFLL 202

Qy         195 PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIA 253
               || :| : |::::      :: ::| |:      :|::| |::| : :|||::|  |
Db         203 PLLIMSYCYFRIIQTLFSCKNHKKAKAI------KLILLVVIVFFLFWTPYNVMIFLETL 256

Qy         254 SRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
                  | :|    :| ::   ::|  :|| :  :||: |   |: :|  |   :  | | !
Db         257 KLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYL---YHLYGKCL 312
```

RESULT 10
US-09-299-843A-28
; Sequence 28, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,843A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/088,337
; FILING DATE: 01-JUN-1998

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;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/153,848
;       FILING DATE:  17-NOV-1993
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/977,452
;       FILING DATE:  17-NOV-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jill E. Uhl
;       REGISTRATION NUMBER:  43,213
;       REFERENCE/DOCKET NUMBER:  27866/32059B
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (312) 474-6300
;       TELEFAX:  (312) 474-0448
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  28:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  355 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-299-843A-28

  Query Match             21.4%;  Score 353;  DB 3;  Length 355;
  Best Local Similarity   28.1%;  Pred. No. 1.5e-21;
  Matches   84;  Conservative   66;  Mismatches  133;  Indels   16;  Gaps    6;

Qy          16 ILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPIL 75
               :    :|| ||:: |  ||:||: |||      |  : :::|| ||::||  |: |||
Db          28 VFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSDLLFVATLPFW 87

Qy          76 IKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA 135
                    |:|| : : :|           : || |:| ||:|||| :          :  :
Db          88 THYLINEKGLH-NAMCKFTTAFFFIGFFGSIFFITVISIDRYLAIVLAANSMNNRTVQHG 146

Qy         136 ILISLAVWALVTLEVLPMLTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLI 194
               : ||| |||   |   |   |     |:: : |: ||          :: ::    ||||:
Db         147 VTISLGVWAAAILVAAPQFMF----TKQKENECLGDYPEVLQEIWPVLRNVETNFLGFLL 202

Qy         195 PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIA 253
               || :| : |::::      :: ::| |:      :|::| |::| : :|||::|  |
Db         203 PLLIMSYCYFRIIQTLFSCKNHKKAKAI------KLILLVVIVFFLFWTPYNVMIFLETL 256

Qy         254 SRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
                 | :|    :| ::   ::|  :|| :  :||: |   |: :|  |   :  | | |
Db         257 KLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYL---YHLYGKCL 312


RESULT 11
US-09-299-843A-32
; Sequence 32, Application US/09299843A
; Patent No. 6107475
;  GENERAL INFORMATION:
;    APPLICANT:  Godiska, Ronald
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Schweikart, Vicki L.
;    TITLE OF INVENTION:  No. 6107475el Seven Transmembrane Receptors
;    NUMBER OF SEQUENCES:  66
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/299,843A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/088,337
;      FILING DATE:  01-JUN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/153,848
;      FILING DATE:  17-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/977,452
;      FILING DATE:  17-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jill E. Uhl
;      REGISTRATION NUMBER:  43,213
;      REFERENCE/DOCKET NUMBER:  27866/32059B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-299-843A-32

  Query Match             21.4%;  Score 353;  DB 3;  Length 355;
  Best Local Similarity   28.1%;  Pred. No. 1.5e-21;
  Matches   84;  Conservative   66;  Mismatches  133;  Indels   16;  Gaps    6;

Qy          16 ILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPIL 75
               :    :|| ||:: |  ||:||: |||      |  : :::|| ||::||  |: |||
Db          28 VFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSDLLFVATLPFW 87

Qy          76 IKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA 135
                 |:|| : : :|           : || |:| ||:|||| :         :  :
Db          88 THYLINEKGLH-NAMCKFTTAFFFIGFFGSIFFITVISIDRYLAIVLAANSMNNRTVQHG 146

Qy         136 ILISLAVWALVTLEVLPMLTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLI 194
               : ||| |||   |   |   |     |:: : |: ||         :: ::    ||||:
Db         147 VTISLGVWAAAILVAAPQFMF----TKQKENECLGDYPEVLQEIWPVLRNVETNFLGFLL 202
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Qy        195 PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIA 253
              || :| : |::::      :: ::| |:      :|::| |::| : :|||::|  |
Db        203 PLLIMSYCYFRIIQTLFSCKNHKKAKAI------KLILLVVIVFFLFWTPYNVMIFLETL 256

Qy        254 SRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
                | :|    :| ::   ::|  :|| :  :||: |   |: :|  |   :  | | |
Db        257 KLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYL---YHLYGKCL 312


RESULT 12
US-09-088-337B-28
; Sequence 28, Application US/09088337B
; Patent No. 6348574
;   GENERAL INFORMATION:
;        APPLICANT: Godiska, Ronald
;                   Gray, Patrick W.
;                   Schweikart, Vicki L.
;        TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
;        NUMBER OF SEQUENCES: 66
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
;                        Borun
;             STREET: 6300 Sears Tower, 233 South Wacker Drive
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60606
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/088,337B
;             FILING DATE: 01-Jun-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/153,848
;             FILING DATE: 17-NOV-1993
;             APPLICATION NUMBER: US 07/977,452
;             FILING DATE: 17-NOV-1992
;        ATTORNEY/AGENT INFORMATION:
;             NAME: No. 6348574and, Greta E.
;             REGISTRATION NUMBER: 35,302
;             REFERENCE/DOCKET NUMBER: 31794
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (312) 474-6300
;             TELEFAX: (312) 474-0448
;             TELEX: 25-3856
;   INFORMATION FOR SEQ ID NO: 28:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 355 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 28:
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US-09-088-337B-28

Query Match 21.4%; Score 353; DB 4; Length 355;
Best Local Similarity 28.1%; Pred. No. 1.5e-21;
Matches 84; Conservative 66; Mismatches 133; Indels 16; Gaps 6;

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Qy          76 IKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA 135
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Db         147 VTISLGVWAAAILVAAPQFMF----TKQKENECLGDYPEVLQEIWPVLRNVETNFLGFLL 202

Qy         195 PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIA 253
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Db         203 PLLIMSYCYFRIIQTLFSCKNHKKAKAI------KLILLVVIVFFLFWTPYNVMIFLETL 256

Qy         254 SRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
                 | :|    :| ::   ::|  :|| :  :||: |   |: :|  |   :  | | |
Db         257 KLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYL---YHLYGKCL 312
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RESULT 13
US-09-088-337B-32
; Sequence 32, Application US/09088337B
; Patent No. 6348574
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; Gray, Patrick W.
; Schweikart, Vicki L.
; TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,843
; FILING DATE: 17-NOV-1993

; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-088-337B-32

Query Match 21.4%; Score 353; DB 4; Length 355;
Best Local Similarity 28.1%; Pred. No. 1.5e-21;
Matches 84; Conservative 66; Mismatches 133; Indels 16; Gaps 6;

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               :    :|| ||:: |  ||:||: |||      |  : :::|| ||::||  |: |||
Db          28 VFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSDLLFVATLPFW 87

Qy          76 IKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA 135
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Qy         136 ILISLAVWALVTLEVLPMLTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLI 194
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Db         147 VTISLGVWAAAILVAAPQFMF----TKQKENECLGDYPEVLQEIWPVLRNVETNFLGFLL 202

Qy         195 PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIA 253
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Db         203 PLLIMSYCYFRIIQTLFSCKNHKKAKAI------KLILLVVIVFFLFWTPYNVMIFLETL 256

Qy         254 SRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
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Db         257 KLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYL---YHLYGKCL 312
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RESULT 14
US-09-170-496D-130
; Sequence 130, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D

; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496D-130

  Query Match   21.4%; Score 353; DB 4; Length 355;
  Best Local Similarity   28.1%; Pred. No. 1.5e-21;
  Matches   84; Conservative   66; Mismatches 133; Indels   16; Gaps   6;

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Db          28 VFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSDLLFVATLPFW 87

Qy          76 IKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA 135
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Qy         136 ILISLAVWALVTLEVLPMLTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLI 194
               : ||| |||   |   |   |     |:: : |: ||          :: ::    ||||:
Db         147 VTISLGVWAAAILVAAPQFMF----TKQKENECLGDYPEVLQEIWPVLRNVETNFLGFLL 202

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Qy         254 SRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
                 | :|    :| ::   ::|  :|| :  :||: |   |: :|  |   :  | | |
Db         257 KLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYL---YHLYGKCL 312
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RESULT 15
US-09-170-496D-232
; Sequence 232, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G
Protein-Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 232
;   LENGTH: 355
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496D-232

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  Best Local Similarity   28.1%;  Pred. No. 1.5e-21;
  Matches   84;  Conservative   66;  Mismatches  133;  Indels   16;  Gaps    6;

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               :    :|| ||:: |  ||:||: |||      |  : :::|| ||::||  |: |||
Db          28 VFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSDLLFVATLPFW 87

Qy          76 IKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA 135
                 |:|| : : :|           : || |:| ||:|||| :         :  :
Db          88 THYLINEKGLH-NAMCKFTTAFFFIGFFGSIFFITVISIDRYLAIVLAANSMNNRTVQHG 146

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Db         147 VTISLGVWAAAILVAAPQFMF----TKQKENECLGDYPEVLQEIWPVLRNVETNFLGFLL 202

Qy         195 PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIA 253
               || :| : |::::      :: ::|      | ::|::| |::| : :|||::|  |
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Qy         254 SRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
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Db         257 KLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYL---YHLYGKCL 312


Search completed: December 12, 2003, 18:09:39
Job time : 22 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 12, 2003, 18:08:37 ; Search time 31 Seconds
(without alignments)
1901.833 Million cell updates/sec

Title: US-09-891-138A-2
Perfect score: 1650
Sequence: 1 MAQNLSCENWLATEAILNKY.....REMLISKFRQYFKSLTSFRT 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	1650	100.0	317	11	US-09-891-138A-2	Sequence 2, Appli
2	1238.5	75.1	330	15	US-10-225-567A-567	Sequence 567, App
3	1238.5	75.1	334	12	US-09-764-886-45	Sequence 45, Appl
4	1238.5	75.1	334	12	US-09-764-886-70	Sequence 70, Appl
5	1238.5	75.1	334	12	US-10-272-983-36	Sequence 36, Appl
6	1238.5	75.1	334	12	US-10-393-807-36	Sequence 36, Appl
7	1231.5	74.6	334	10	US-09-765-034-2	Sequence 2, Appli
8	1224.5	74.2	334	15	US-10-270-587-2	Sequence 2, Appli
9	1141.5	69.2	288	12	US-09-764-886-80	Sequence 80, Appl
10	479	29.0	289	12	US-09-764-886-79	Sequence 79, Appl
11	479	29.0	373	12	US-09-991-225-5	Sequence 5, Appli
12	479	29.0	373	12	US-10-010-568-6	Sequence 6, Appli
13	479	29.0	373	15	US-10-092-135-7	Sequence 7, Appli
14	475	28.8	299	15	US-10-270-144-4	Sequence 4, Appli
15	475	28.8	373	12	US-10-010-568-5	Sequence 5, Appli
16	474	28.7	373	12	US-10-010-568-7	Sequence 7, Appli
17	474	28.7	373	12	US-10-010-568-8	Sequence 8, Appli
18	474	28.7	373	12	US-09-745-842-14	Sequence 14, Appl
19	474	28.7	373	15	US-10-092-135-5	Sequence 5, Appli
20	474	28.7	373	15	US-10-092-135-6	Sequence 6, Appli
21	474	28.7	373	15	US-10-225-567A-219	Sequence 219, App
22	472.5	28.6	362	11	US-09-779-679-28	Sequence 28, Appl
23	472.5	28.6	362	12	US-09-991-225-3	Sequence 3, Appli
24	472.5	28.6	362	12	US-09-991-225-4	Sequence 4, Appli
25	472.5	28.6	362	12	US-10-010-568-3	Sequence 3, Appli
26	472.5	28.6	362	12	US-10-010-568-4	Sequence 4, Appli
27	472.5	28.6	362	12	US-10-044-643-46	Sequence 46, Appl
28	472.5	28.6	362	12	US-10-044-643-47	Sequence 47, Appl
29	472.5	28.6	362	15	US-10-092-135-3	Sequence 3, Appli
30	472.5	28.6	362	15	US-10-092-135-4	Sequence 4, Appli
31	426	25.8	337	9	US-09-943-798-4	Sequence 4, Appli
32	426	25.8	337	11	US-09-885-453-1	Sequence 1, Appli
33	426	25.8	337	12	US-10-017-161-526	Sequence 526, App
34	426	25.8	337	12	US-10-278-141-2	Sequence 2, Appli
35	426	25.8	337	12	US-10-010-568-2	Sequence 2, Appli
36	426	25.8	337	12	US-10-321-807-28	Sequence 28, Appl
37	426	25.8	337	12	US-10-296-081-2	Sequence 2, Appli
38	426	25.8	337	15	US-10-023-775B-2	Sequence 2, Appli
39	426	25.8	337	15	US-10-270-144-2	Sequence 2, Appli
40	426	25.8	337	15	US-10-188-405-8	Sequence 8, Appli
41	426	25.8	337	15	US-10-079-384-14	Sequence 14, Appl
42	422.5	25.6	374	12	US-10-010-568-11	Sequence 11, Appl
43	422.5	25.6	374	12	US-09-745-842-15	Sequence 15, Appl
44	419	25.4	337	15	US-10-225-567A-647	Sequence 647, App
45	386.5	23.4	537	12	US-10-010-568-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-891-138A-2
; Sequence 2, Application US/09891138A
; Publication No. US20030083245A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Daniel Chi-Hong

; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030083245A1el Receptors
; FILE REFERENCE: 018781-006210US
; CURRENT APPLICATION NUMBER: US/09/891,138A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,461
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse TGR18 G-protein coupled receptor (GPCR)
US-09-891-138A-2

Query Match 100.0%; Score 1650; DB 11; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.6e-141;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
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Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
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Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
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Qy        241 FTPYHIMRNLRIASRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREM 300
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Db        241 FTPYHIMRNLRIASRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREM 300

Qy        301 LISKFRQYFKSLTSFRT 317
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Db        301 LISKFRQYFKSLTSFRT 317
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RESULT 2
US-10-225-567A-567
; Sequence 567, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.

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;  APPLICANT:  Roush, Christine L.
;  TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
RECEPTORS (GPCRS)
;  FILE REFERENCE: 1920-4-4
;  CURRENT APPLICATION NUMBER: US/10/225,567A
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/257,144
;  PRIOR FILING DATE: 2000-12-19
;  NUMBER OF SEQ ID NOS: 2292
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 567
;   LENGTH: 330
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-225-567A-567

  Query Match             75.1%;  Score 1238.5;  DB 15;  Length 330;
  Best Local Similarity   72.2%;  Pred. No. 3.3e-104;
  Matches  228;  Conservative   42;  Mismatches   45;  Indels    1;  Gaps    1;

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Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
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Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
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Db        181 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 240

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:|||||| || |  |||  | | | :||||||||| |||:||||:|||:|:
Db        241 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 300

Qy        300 MLISKFRQYFKSLTSF 315
              ||::: |  |||||||
Db        301 MLMNQLRHNFKSLTSF 316


RESULT 3
US-09-764-886-45
; Sequence 45, Application US/09764886
; Publication No. US20030139327A9
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PTZ02
;  CURRENT APPLICATION NUMBER: US/09/764,886
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 88
```

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;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
;   LENGTH: 334
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-764-886-45

  Query Match             75.1%;  Score 1238.5;  DB 12;  Length 334;
  Best Local Similarity   72.2%;  Pred. No. 3.3e-104;
  Matches  228;  Conservative   42;  Mismatches   45;  Indels    1;  Gaps    1;

Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              || | :|:|||| || | ||||| || |||: |:||| ||:||:| :|||||||:||||
Db          5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:|||| ||||||||||||| ||||||||||||:||||::
Db         65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||| |||||||||||||:| |||||:||:|  || |  : |: | |:||||:| :|
Db        125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||:|||||||||| |||||||: :|||:|::| ||||||:|| ||::|||||:|
Db        185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 244

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:|||||| || |  |||  | | | :||||||||| |||:||||:|||:|:
Db        245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304

Qy        300 MLISKFRQYFKSLTSF 315
              ||::: |  |||||||
Db        305 MLMNQLRHNFKSLTSF 320


RESULT 4
US-09-764-886-70
; Sequence 70, Application US/09764886
; Publication No. US20030139327A9
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PTZ02
;  CURRENT APPLICATION NUMBER: US/09/764,886
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 88
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
;   LENGTH: 334
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-764-886-70

  Query Match             75.1%;  Score 1238.5;  DB 12;  Length 334;
  Best Local Similarity   72.2%;  Pred. No. 3.3e-104;
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  Matches  228;  Conservative   42;  Mismatches   45;  Indels    1;  Gaps    1;

Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              ||  | :|:|||| ||  | ||||| ||  ||| |:||| ||:||:| :|||||||:|||| 
Db          5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:||||    |||||||||||||| ||||||||||||:||||:: 
Db         65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||| |||||||||||||:| |||||:||:|  || |  : |: | |:||||:| :| 
Db        125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||:|||||||||| ||||||||: :|||:|::| ||||||:||  ||::||||||:| 
Db        185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 244

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:|||||| ||  |  |||  | | | :||||||||| |||:||||:|||:|: 
Db        245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304

Qy        300 MLISKFRQYFKSLTSF 315
              ||::: |  ||||||| 
Db        305 MLMNQLRHNFKSLTSF 320
```

RESULT 5
US-10-272-983-36
; Sequence 36, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439

; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
;   LENGTH: 334
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-272-983-36

  Query Match 75.1%; Score 1238.5; DB 12; Length 334;
  Best Local Similarity 72.2%; Pred. No. 3.3e-104;
  Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

```
Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              ||  |  :|:|||| ||  |  ||||| ||  |||: |:|||  ||:||:|  :|||||||:||||
Db          5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:||  |||||||:||:||||     |||||||||||||| ||||||||||||:||||::
Db         65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              |||||||  ||||||||||||:|  |||||:||:|   ||  |   :  |:  |  |:||||:|  :|
Db        125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||:|||||||||||  ||||||||:  :|||:|::|  ||||||:||   ||::|||||||:|
Db        185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 244

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:||||||  ||  |  |||  |  |  |  :|||||||||  |||:||||:|||:|:
Db        245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304

Qy        300 MLISKFRQYFKSLTSF 315
              ||:::  |  |||||||
Db        305 MLMNQLRHNFKSLTSF 320
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RESULT 6
US-10-393-807-36
; Sequence 36, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213

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;  PRIOR FILING DATE: 1998-11-20
;  PRIOR APPLICATION NUMBER: 60/120,416
;  PRIOR FILING DATE: 1999-02-16
;  PRIOR APPLICATION NUMBER: 60/121,851
;  PRIOR FILING DATE: 1999-02-26
;  PRIOR APPLICATION NUMBER: 60/123,946
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/123,949
;  PRIOR FILING DATE: 1999-03-12
;  PRIOR APPLICATION NUMBER: 60/136,436
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/136,437
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/136,439
;  PRIOR FILING DATE: 1999-05-28
;  PRIOR APPLICATION NUMBER: 60/136,567
;  PRIOR FILING DATE: 1999-05-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
;   LENGTH: 334
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-393-807-36

  Query Match             75.1%;  Score 1238.5;  DB 12;  Length 334;
  Best Local Similarity   72.2%;  Pred. No. 3.3e-104;
  Matches  228;  Conservative   42;  Mismatches   45;  Indels    1;  Gaps    1;

Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              || | :|:|||| || | ||||| || |||: |:||| ||:||:| :|||||||:||||
Db          5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:|||| |||||||||||||| ||||||||||||:||||::
Db         65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||| |||||||||||||:| |||||:||:| || | : |: | |:||||:| :|
Db        125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||:|||||||||| |||||||: :|||:|::| ||||||:|| ||::||||||:|
Db        185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 244

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:|||||| || |  |||  | | | :||||||||| |||:||||:|||:|:
Db        245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304

Qy        300 MLISKFRQYFKSLTSF 315
              ||::: |  |||||||
Db        305 MLMNQLRHNFKSLTSF 320


RESULT 7
US-09-765-034-2
```

; Sequence 2, Application US/09765034
; Patent No. US20020137887A1
; GENERAL INFORMATION:
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Lachowicz, Jean E.
; APPLICANT: Wang, Wei
; APPLICANT: Gustafson, Eric L.
; TITLE OF INVENTION: Adenosine Receptor
; FILE REFERENCE: CN01084
; CURRENT APPLICATION NUMBER: US/09/765,034
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 334
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-765-034-2

  Query Match 74.6%; Score 1231.5; DB 10; Length 334;
  Best Local Similarity 71.8%; Pred. No. 1.4e-103;
  Matches 227; Conservative 42; Mismatches 46; Indels 1; Gaps 1;

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Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              ||  |  :|:|||| ||  |  ||||| ||  ||| |:|||  ||:||:|  :|||||||:||||
Db          5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:||||    |||||||||||||| ||||||||||||:||||::
Db         65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              |||||||  |||||||||||||:|  |||||:||:|  ||  |  :  |:  |  |:|||||:|  :|
Db        125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||:||||||||||| ||||||||: :|||:|::|  ||||||:||   ||::||||||:
Db        185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVP 244

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:|||||| ||  |  |||  |  |  |  :|||||||| |||:||||:|||:|:
Db        245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304

Qy        300 MLISKFRQYFKSLTSF 315
              ||::: |  |||||||
Db        305 MLMNQLRHNFKSLTSF 320
```

RESULT 8
US-10-270-587-2
; Sequence 2, Application US/10270587
; Publication No. US20030054487A1
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; TITLE OF INVENTION: Human G-Protein Coupled Receptor
; FILE REFERENCE: PF217C2
; CURRENT APPLICATION NUMBER: US/10/270,587

```
;  CURRENT FILING DATE:  2002-10-16
;  PRIOR APPLICATION NUMBER: US 09/908,593
;  PRIOR FILING DATE: 2001-07-20
;  PRIOR APPLICATION NUMBER: US 08/781,456
;  PRIOR FILING DATE: 1997-01-10
;  PRIOR APPLICATION NUMBER: US 60/009,902
;  PRIOR FILING DATE: 1996-01-11
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 334
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-270-587-2

  Query Match             74.2%;  Score 1224.5;  DB 15;  Length 334;
  Best Local Similarity   71.5%;  Pred. No. 6.2e-103;
  Matches  226;  Conservative   43;  Mismatches   46;  Indels    1;  Gaps    1;

Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              || | :|:|||| || | ||||| || |||: |:||| ||:||:| :||||||:||||
Db          5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:|||| ||||||||||||| ||||||||||||:|||::
Db         65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||| ||||| |||||||:| |||||:||:|  || |  : |: | |:||||:| :|
Db        125 KYPFREHLLQKKECAILISLAMWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||:|||||||||||| |||||||: :|||:|::| ||||||:||  ||::|||||:|
Db        185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 244

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:|||||| || |  |||  | | | :|||:||||| |||:||||:|||:|:
Db        245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPVAFLNSVINPVFYFLVGDHFRD 304

Qy        300 MLISKFRQYFKSLTSF 315
              ||::: |  |||||||
Db        305 MLMNQLRHNFKSLTSF 320


RESULT 9
US-09-764-886-80
; Sequence 80, Application US/09764886
; Publication No. US20030139327A9
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PTZ02
;  CURRENT APPLICATION NUMBER: US/09/764,886
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 88
;  SOFTWARE: PatentIn Ver. 2.0
```

; SEQ ID NO 80
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-886-80

  Query Match 69.2%; Score 1141.5; DB 12; Length 288;
  Best Local Similarity 72.6%; Pred. No. 1.7e-95;
  Matches 209; Conservative 40; Mismatches 38; Indels 1; Gaps 1;

```
Qy         20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
              |||| || |||: |:|||  ||:||:| :|||||||:||||||:|| |||||||:||:||
Db          1 YYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFNLSVSDLAFLCTLPMLIRSY 60

Qy         80 ANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILIS 139
              ||    |||||||||||||| ||||||||||||:||||::|||||| ||||||||||
Db         61 ANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLIIKYPFREHLLQKKEFAILIS 120

Qy        140 LAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
              ||:| |||||:||:|  || |  : |: | |:||||:| :||||:|||||||||| ||
Db        121 LAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYNLIYSMCLTLLGFLIPLFVM 180

Qy        200 CFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIASRLDSW 259
              ||||||: :|||:|::| |||||||:||  ||::||||||:||||||:|||:|||||| ||
Db        181 CFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVLFTPYHVMRNVRIASRLGSW 240

Qy        260 PQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFR 306
               |  |||  | | | :||||||||| |||:||||:|||:|:||::: |
Db        241 KQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRDMLMNQLR 288
```

RESULT 10
US-09-764-886-79
; Sequence 79, Application US/09764886
; Publication No. US20030139327A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ02
; CURRENT APPLICATION NUMBER: US/09/764,886
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-886-79

  Query Match 29.0%; Score 479; DB 12; Length 289;
  Best Local Similarity 37.3%; Pred. No. 1.8e-35;
  Matches 107; Conservative 57; Mismatches 115; Indels 8; Gaps 6;

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Qy         20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
              ||| | | : || | |||   :: ::| || |:  :||:|||:::|| :: ||| ||  |
Db          1 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 60
```

```
Qy          80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
                 |     :|||:|   |:: | ||| |||||| ||  ||  : || :     ||: || :
Db          61 FNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAIYV 120

Qy         139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
               |: || :| : : |:| :  : : | :   | |  |        |||:| |:  | |||
Db         121 SVLVWLIVVVAISPILFYSGTGIRKNKTVTCYDSTSDEYLRSYFIYSMCTTVAMFCIPLV 180

Qy         198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
               ::   | :|  |  :   :   ||  |   ||:: : :|:: : |:|:|: : : :||
Db         181 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 237

Qy         257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
               |   |: |     : : | :|| || ||| ::|| ||| || :|  |
Db         238 DFQTPEMCDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 284


RESULT 11
US-09-991-225-5
; Sequence 5, Application US/09991225
; Publication No. US20030153063A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11,
EXPRESSED HIGHLY IN
;  TITLE OF INVENTION:  HEART AND VARIANTS THEREOF
;  FILE REFERENCE: D0075.NP
;  CURRENT APPLICATION NUMBER: US/09/991,225
;  CURRENT FILING DATE:  2001-11-16
;  PRIOR APPLICATION NUMBER: 60/249,613
;  PRIOR FILING DATE: 2000-11-17
;  PRIOR APPLICATION NUMBER: 60/257,611
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: 60/305,818
;  PRIOR FILING DATE: 2001-07-16
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 373
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-991-225-5

  Query Match           29.0%;  Score 479;  DB 12;  Length 373;
  Best Local Similarity   37.3%;  Pred. No. 2.5e-35;
  Matches  107;  Conservative   57;  Mismatches  115;  Indels    8;  Gaps    6;

Qy          20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
               ||| | | : || | |||   :: ::| || |:  :||:|||:::|| :: ||| ||  |
Db          52 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 111

Qy          80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
                 |     :|||:|   |:: | ||| |||||| ||  ||  : || :     ||: || :
Db         112 FNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAIYV 171

Qy         139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
```

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                |: || :| : : |:| :  : : | :   | |  |        |||:| |:  | |||
Db        172 SVLVWLIVVVAISPILFYSGTGIRKNKTVTCYDSTSDEYLRSYFIYSMCTTVAMFCIPLV 231

Qy        198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
              ::   |  :|  |  :    :   ||  |   ||:: : :|:: : |:|:|: : : :||
Db        232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 288

Qy        257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
              |   |: |     : : | :|| || ||| ::|| ||| || :|  |
Db        289 DFQTPEMCDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335


RESULT 12
US-10-010-568-6
; Sequence 6, Application US/10010568
; Publication No. US20030157598A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY23,
EXPRESSED HIGHLY IN
;  TITLE OF INVENTION:  KIDNEY
;  FILE REFERENCE: D0077 NP
;  CURRENT APPLICATION NUMBER: US/10/010,568
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: US 60/251,926
;  PRIOR FILING DATE: 2000-12-07
;  PRIOR APPLICATION NUMBER: US 60/269,795
;  PRIOR FILING DATE: 2001-02-14
;  NUMBER OF SEQ ID NOS: 55
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 373
;   TYPE: PRT
;   ORGANISM: RATTUS NORVEGICUS
US-10-010-568-6

  Query Match           29.0%;  Score 479;  DB 12;  Length 373;
  Best Local Similarity  37.3%;  Pred. No. 2.5e-35;
  Matches  107;  Conservative   57;  Mismatches  115;  Indels    8;  Gaps    6;

Qy         20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
              ||| | | : || | |||   :: ::| || |:  :||:|||:::|| :: ||| ||  |
Db         52 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 111

Qy         80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
               |     :|||:|   |:: | ||| |||||| ||  ||  : || :     ||: || :
Db        112 FNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAIYV 171

Qy        139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
              |: || :| : : |:| :  : : | :   | |  |        |||:| |:  | |||
Db        172 SVLVWLIVVVAISPILFYSGTGIRKNKTVTCYDSTSDEYLRSYFIYSMCTTVAMFCIPLV 231

Qy        198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
              ::   |  :|  |  :    :   ||  |   ||:: : :|:: : |:|:|: : : :||
Db        232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 288

Qy        257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
```

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                |   |: |     : : | :|| || ||| ::|| ||| || :|  |
Db        289 DFQTPEMCDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335


RESULT 13
US-10-092-135-7
; Sequence 7, Application US/10092135
; Publication No. US20030054374A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED
RECEPTOR,
;  TITLE OF INVENTION: HGPRBMY27
;  FILE REFERENCE: D0134.NP
;  CURRENT APPLICATION NUMBER: US/10/092,135
;  CURRENT FILING DATE:  2002-03-06
;  PRIOR APPLICATION NUMBER: US 60/273,808
;  PRIOR FILING DATE: 2001-03-07
;  PRIOR APPLICATION NUMBER: US 60/278,983
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 373
;   TYPE: PRT
;   ORGANISM: RATTUS NORVEGICUS
US-10-092-135-7

  Query Match             29.0%;  Score 479;  DB 15;  Length 373;
  Best Local Similarity   37.3%;  Pred. No. 2.5e-35;
  Matches  107;  Conservative   57;  Mismatches  115;  Indels    8;  Gaps    6;

Qy         20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
              ||| | | : || | |||   :: ::| || |:  :||:|||:::|| :: ||| || |
Db         52 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 111

Qy         80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
               |     :|||:|   |:: | ||| |||||| ||  ||  : || :     ||: || :
Db        112 FNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAIYV 171

Qy        139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
              |: || :| : : |:| :  : : | :   | |  |        |||:| |:  | |||
Db        172 SVLVWLIVVVAISPILFYSGTGIRKNKTVTCYDSTSDEYLRSYFIYSMCTTVAMFCIPLV 231

Qy        198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
              ::   | :|  |  :    :   ||  |   ||:: : :|:: : |:|:|: : : :||
Db        232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 288

Qy        257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
              |   |: |     : : | :|| || ||| ::|| ||| || :|  |
Db        289 DFQTPEMCDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335


RESULT 14
US-10-270-144-4
; Sequence 4, Application US/10270144
; Publication No. US20030049790A1
```

; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000750CON
; CURRENT APPLICATION NUMBER: US/10/270,144
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/205,196
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-270-144-4

Query Match 28.8%; Score 475; DB 15; Length 299;
Best Local Similarity 37.3%; Pred. No. 4.4e-35;
Matches 107; Conservative 55; Mismatches 117; Indels 8; Gaps 7;

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Qy          20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
               ||| | | : || | |||   :: ::| || |:  :||:|||:::|| :: ||| ||  |
Db          11 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 70

Qy          80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
                |     :|| :|   |:: | ||| |||||| ||  ||  : || :     ||: || :
Db          71 FNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAIYV 130

Qy         139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
               |: || :| : : |:| :  :   | :   | |  |:       |||:| |:  | |||
Db         131 SVLVWLIVVVAISPILFYSGTGTRKNKTVTCYDTTSNDYLRSYFIYSMCTTVAMFCIPL- 189

Qy         198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
               |:    | ::|  |          ||  |   ||:: : :|:: : |:|:|: : : :||
Db         190 VLILGCYGLIV--KALIYNDLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 247

Qy         257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
               |   |: |     : : | :|| || ||| ::|| ||| || :|  |
Db         248 DFQTPEMCDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 294
```

RESULT 15
US-10-010-568-5
; Sequence 5, Application US/10010568
; Publication No. US20030157598A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY23,
EXPRESSED HIGHLY IN
; TITLE OF INVENTION: KIDNEY
; FILE REFERENCE: D0077 NP
; CURRENT APPLICATION NUMBER: US/10/010,568
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/251,926
; PRIOR FILING DATE: 2000-12-07

```
;  PRIOR APPLICATION NUMBER: US 60/269,795
;  PRIOR FILING DATE: 2001-02-14
;  NUMBER OF SEQ ID NOS: 55
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 373
;   TYPE: PRT
;   ORGANISM: MUS MUSCULUS
US-10-010-568-5

  Query Match             28.8%;  Score 475;  DB 12;  Length 373;
  Best Local Similarity   37.3%;  Pred. No. 5.7e-35;
  Matches  107;  Conservative   55;  Mismatches  117;  Indels    8;  Gaps    7;

Qy         20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
              ||| | | : || | |||   :: ::| || |:  :||:|||:::|| :: ||| ||  |
Db         52 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 111

Qy         80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
               |     :|| :|   |:: | ||| |||||| ||  ||  : || :     ||: || :
Db        112 FNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAIYV 171

Qy        139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
              |: || :| : : |:| :  :   | :   | |  |:       |||:| |:  | |||
Db        172 SVLVWLIVVVAISPILFYSGTGTRKNKTVTCYDTTSNDYLRSYFIYSMCTTVAMFCIPL- 230

Qy        198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
              |:    | ::|  |          ||  |   ||:: : :|:: : |:|:|: : : :||
Db        231 VLILGCYGLIV--KALIYNDLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 288

Qy        257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
              |   |: |     : : | :|| || ||| ::|| ||| || :|  |
Db        289 DFQTPEMCDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335


Search completed: December 12, 2003, 18:14:04
Job time : 32 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 12, 2003, 18:04:37 ; Search time 40 Seconds
(without alignments)
2045.067 Million cell updates/sec

Title: US-09-891-138A-2
Perfect score: 1650
Sequence: 1 MAQNLSCENWLATEAILNKY.....REMLISKFRQYFKSLTSFRT 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	1634	99.0	317	11	Q99MT6	Q99mt6 mus musculu
2	1238.5	75.1	330	4	Q9BXA5	Q9bxa5 homo sapien
3	1238.5	75.1	334	4	Q8TDQ8	Q8tdq8 homo sapien
4	482.5	29.2	361	13	Q90X57	Q90x57 xenopus lae
5	479	29.0	373	11	Q8BMJ5	Q8bmj5 mus musculu
6	461	27.9	357	13	Q9DE05	Q9de05 raja erinac
7	426	25.8	337	4	Q96P68	Q96p68 homo sapien
8	422.5	25.6	374	13	O57466	O57466 meleagris g
9	353	21.4	361	11	Q8VHP3	Q8vhp3 cavia porce
10	343	20.8	360	6	Q8MJW8	Q8mjw8 canis famil
11	338	20.5	328	11	Q9ERK9	Q9erk9 mus musculu
12	335	20.3	355	6	Q9MYJ8	Q9myj8 callithrix
13	333	20.2	355	11	Q9JLY8	Q9jly8 rattus norv
14	326.5	19.8	354	11	Q8CBJ0	Q8cbj0 mus musculu
15	326	19.8	351	6	Q9MYJ9	Q9myj9 oryctolagus
16	325.5	19.7	354	11	Q8BR50	Q8br50 mus musculu
17	323.5	19.6	360	11	Q91ZH4	Q91zh4 rattus norv
18	321	19.5	344	11	Q8BMC0	Q8bmc0 mus musculu
19	318.5	19.3	309	11	Q8R528	Q8r528 mus musculu
20	317.5	19.2	355	6	Q8HZN7	Q8hzn7 gorilla gor
21	316.5	19.2	355	6	Q95LH1	Q95lh1 macaca fasc
22	316.5	19.2	385	11	Q8BQ97	Q8bq97 mus musculu
23	316	19.2	367	13	Q9PVG0	Q9pvg0 carassius a
24	315	19.1	355	4	Q9BYX5	Q9byx5 homo sapien
25	314	19.0	356	4	Q96TF2	Q96tf2 homo sapien
26	313	19.0	355	11	Q8BVW4	Q8bvw4 mus musculu
27	313	19.0	355	11	Q8BMH9	Q8bmh9 mus musculu
28	313	19.0	367	13	Q9PVF9	Q9pvf9 carassius a
29	312.5	18.9	346	4	Q96GE0	Q96ge0 homo sapien
30	312.5	18.9	355	4	Q8IUZ1	Q8iuz1 homo sapien
31	312.5	18.9	355	6	Q8HZN8	Q8hzn8 pan trcglod
32	312.5	18.9	390	13	Q8QGQ4	Q8qgq4 carassius a
33	310.5	18.8	339	4	Q8N5S7	Q8n5s7 homo sapien
34	310	18.8	370	11	Q8BKK1	Q8bkk1 mus musculu
35	309.5	18.8	355	6	Q8HZN3	Q8hzn3 papio hamad
36	308.5	18.7	355	6	Q8HZN4	Q8hzn4 cercopithec
37	308	18.7	346	11	Q91Y73	Q91y73 mus musculu
38	307.5	18.6	390	13	Q8AXM7	Q8axm7 carassius a
39	307	18.6	362	4	Q8NE10	Q8ne10 homo sapien
40	307	18.6	375	11	Q8BYI1	Q8byi1 mus musculu
41	306.5	18.6	355	6	Q8HZN6	Q8hzn6 pongo pygma
42	306.5	18.6	392	6	Q9BDQ4	Q9bdq4 canis famil
43	306	18.5	337	11	Q921N3	Q921n3 mus musculu
44	306	18.5	370	11	Q8BLG2	Q8blg2 mus musculu
45	304	18.4	343	13	Q8JJ23	Q8jj23 oncorhynchu

ALIGNMENTS

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RESULT 1
Q99MT6
ID   Q99MT6       PRELIMINARY;      PRT;   317 AA.
AC   Q99MT6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
```

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DE   G-protein coupled receptor GPR91.
GN   GPR91.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL;
RX   MEDLINE=21172992; PubMed=11273702;
RA   Wittenberger T., Schaller H.C., Hellebrand S.;
RT   "An expressed sequence tag (est) data mining strategy succeeding in
RT   the discovery of new g-protein coupled receptors.";
RL   J. Mol. Biol. 307:799-813(2001).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF295367; AAK01867.1; -.
DR   MGD; MGI:1934135; Gpr91.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   317 AA;  36701 MW;  4E22F0608F928E36 CRC64;

  Query Match           99.0%;  Score 1634;  DB 11;  Length 317;
  Best Local Similarity  99.1%;  Pred. No. 8.6e-132;
  Matches  314;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||||||||||||||||||||||||||||||||||||||||:| || |||||||||
Db         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSMLLLTVISMDRYLLM 120

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240

Qy        241 FTPYHIMRNLRIASRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FTPYHIMRNLRIASRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREM 300

Qy        301 LISKFRQYFKSLTSFRT 317
              |||||||||||||||||
Db        301 LISKFRQYFKSLTSFRT 317


RESULT 2
Q9PXA5
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ID   Q9BXA5      PRELIMINARY;      PRT;   330 AA.
AC   Q9BXA5;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   G-protein coupled receptor 91.
GN   GPR91.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21172992; PubMed=11273702;
RA   Wittenberger T., Schaller H.C., Hellebrand S.;
RT   "An expressed sequence tag (est) data mining strategy succeeding in
RT   the discovery of new g-protein coupled receptors.";
RL   J. Mol. Biol. 307:799-813(2001).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF348078; AAK29080.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   330 AA;  38283 MW;  6D3C70E340866BAB CRC64;

  Query Match             75.1%;  Score 1238.5;  DB 4;  Length 330;
  Best Local Similarity   72.2%;  Pred. No. 5.7e-98;
  Matches  228;  Conservative   42;  Mismatches   45;  Indels    1;  Gaps    1;

Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              || | :|:|||| || | ||||| || |||: |:||| ||:||:| :||||||:||||
Db          1 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 60

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:|||| |||||||||||| ||||||||||||:||||::
Db         61 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 120

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||| |||||||||||||:| |||||:||:|  || |  : |: | |:||||:| :|
Db        121 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 180

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||:|||||||||||| |||||||: :|||:|::| ||||||:|| ||::||||||:|
Db        181 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 240

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:||||| || |  |||  | | | :|||||||| |||:||||:|||:|:
Db        241 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 300

Qy        300 MLISKFRQYFKSLTSF 315
              ||::: |  |||||||
Db        301 MLMNQLRHNFKSLTSF 316
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RESULT 3
Q8TDQ8
ID   Q8TDQ8      PRELIMINARY;      PRT;   334 AA.
AC   Q8TDQ8;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   P2Y purinoceptor 1 (G protein-coupled receptor 91).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang W., Li N., Wan T., Cao X.;
RT   "Human P2Y purinoceptor 1.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR   EMBL; AF247785; AAL95690.1; -.
DR   EMBL; BC030948; AAH30948.1; -.
DR   Genew; HGNC:4542; GPR91.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   334 AA;  38697 MW;  33146E1AD87F0E81 CRC64;

  Query Match           75.1%;  Score 1238.5;  DB 4;  Length 334;
  Best Local Similarity  72.2%;  Pred. No. 5.8e-98;
  Matches  228;  Conservative   42;  Mismatches   45;  Indels    1;  Gaps    1;

Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              || | :|:|||| || | ||||| || |||: |:||| ||:||:| :|||||||:||||
Db          5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:|||| |||||||||||||| ||||||||||||:||||::
Db         65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||| |||||||||||||:| |||||:||:|  || |  : |: | |:||||:| :|
Db        125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||:|||||||||| |||||||| :|||:|::| ||||||:||  ||::||||||:|
Db        185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 244

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:|||||| || |  |||  | | | :|||||||| |||:||||:|||:|:
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Db        245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304

Qy        300 MLISKFRQYFKSLTSF 315
              ||::: |  |||||||
Db        305 MLMNQLRHNFKSLTSF 320


RESULT 4
Q90X57
ID   Q90X57      PRELIMINARY;      PRT;   361 AA.
AC   Q90X57;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   P2Y1 nucleotide receptor.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cheng A.W., Tsim K.W.;
RT   "Cloning of Xenopus P2Y1 Receptor.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF432354; AAL27614.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   361 AA;  41002 MW;  E5B2D605F5B57FED CRC64;

  Query Match             29.2%;  Score 482.5;  DB 13;  Length 361;
  Best Local Similarity   36.7%;  Pred. No. 2.6e-33;
  Matches  114;  Conservative   58;  Mismatches  124;  Indels   15;  Gaps   8;

Qy          1 MAQNLSCENWLATEAILNK-----YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSN 55
              :|   |  |   |:  | |     |||| | | :  | | :||   :: ::| || |:| :
Db         18 LASGSSAGN--VTKCSLTKTGFQFYYLPAVYIVVCITGFIGNSVAIWMFIFHMKPWSSIS 75

Qy         56 VYLFNLSISDFAFLCTLPILIKSYANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISM 114
              ||:|||:::|| :: :|| ||  | |     :|| ||   |:: | ||| |||||| ||:
Db         76 VYMFNLALADFLYVLSLPALIFYYFNKTDWIFGDALCKLQRFLFHVNLYGSILFLTCISV 135

Qy        115 DRYLLMKYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYAS 173
               ||  : :| :     ||: :| ||  || :|   : |:| |  : : | :   | | :|
Db        136 HRYTGVVHPLKSLGRLKKKNSIYISALVWFIVIAGISPILFFSGTGIRKNKTITCFDTSS 195

Qy        174 SGNPEHNLIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQ-RLVVL 232
                  |||:| |: || ||  ::   |  :|  |  :    |   || |    ||::
Db        196 DEYLRSYFIYSMCTTVFGFCIPFILILGCYGLIVRALIYKDMNNA---PLRKKSIYLVII 252

Qy        233 AVVIFSILFTPYHIMRNLRIASRLD-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFY 290
               : :|:: : |:|:|:|| : :|||   |: |     : : | :|| || ||| ::|| |
Db        253 VLTVFAVSYLPFHVMKNLNLRARLDFQSPEMCNFNDRVYATYQVTRGLASLNSCVDPILY 312
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Qy          291 FLMGDHYREML 301
                || || :|  |
Db          313 FLAGDTFRRKL 323


RESULT 5
Q8BMJ5
ID   Q8BMJ5      PRELIMINARY;      PRT;   373 AA.
AC   Q8BMJ5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   P2Y purinoceptor 1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Body;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK030759; BAC27125.1; -.
SQ   SEQUENCE   373 AA;  42228 MW;  BA38124B7347287C CRC64;

  Query Match          29.0%;  Score 479;  DB 11;  Length 373;
  Best Local Similarity  37.6%;  Pred. No. 5.3e-33;
  Matches  108;  Conservative   54;  Mismatches  117;  Indels    8;  Gaps    7;

Qy           20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
                ||| | | : || | |||   :: |:| || |:  :||:|||:::|| :: ||| ||  |
Db           52 YYLPAVYILVFIIGFLGNSVAIWMYVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 111

Qy           80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
                |     :|| :|   |:: | ||| |||||| ||  ||  : || :     ||: || :
Db          112 FNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAIYV 171

Qy          139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
                |: || :| : : |:| :  :   | :   | |  |:       |||:| |:  | |||
Db          172 SVLVWLIVVVAISPILFYSGTGTRKNKTVTCYDTTSNDYLRSYFIYSMCTTVAMFCIPL- 230

Qy          198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
                |:    | ::|  |           ||  |  ||:: : :|:: : |:|:|: : : :||
Db          231 VLILGCYGLIV--KALIYNDLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 288

Qy          257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
                |   |: |     : : | :|| || ||| ::|| ||| || :|  |
Db          289 DFQTPEMCDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335


RESULT 6
Q9DE05
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ID   Q9DE05      PRELIMINARY;      PRT;   357 AA.
AC   Q9DE05;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   P2Y receptor.
OS   Raja erinacea (Little skate).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC   Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
OC   Rajiformes; Rajidae; Raja.
OX   NCBI_TaxID=7782;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20459151; PubMed=10900200;
RA   Dranoff J.A., O'Neill A.F., Franco A.M., Cai S.Y., Connolly G.C.,
RA   Ballatori N., Boyer J.L., Nathanson M.H.;
RT   "A primitive ATP receptor from the little skate Raja erinacea.";
RL   J. Biol. Chem. 275:30701-30706(2000).
DR   EMBL; AF242850; AAG42684.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   357 AA;  41239 MW;  14604EE15DCBDB41 CRC64;

  Query Match             27.9%;  Score 461;  DB 13;  Length 357;
  Best Local Similarity   35.0%;  Pred. No. 1.8e-31;
  Matches  110;  Conservative   64;  Mismatches  112;  Indels   28;  Gaps   11;

Qy         17 LNK----YYLSAFYAIEFIFGLLGNVIVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTL 72
              |||    |||   | | |: | :||   :: ::| |: |:|  :|:||| ::|  :: :|
Db         29 LNKGFQFYYLPIMYIIVFVTGFIGNSVALWMFIFHMRPWSSITIYMFNLVLADLFYVFSL 88

Qy         73 PILIKSYANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQK 131
              ||||  | |     :|::||   |:: | ||| ||||| ||: ||  : :| :     |
Db         89 PILIFYYFNKTDWIFGELLCKLXRFIFHVNLYGSILFLTCISVHRYTGVVHPMKSLGRLK 148

Qy        132 KEFAILISLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLL 190
              |: | :: : ||  |   : |:| | : : : : : | |  |    |   |||:  |
Db        149 KKSATIVCVCVWITVMAGISPILYFSRTGLRRNKTNTCYDTTSKELLETYFIYSMSTTFF 208

Qy        191 GFLIPLS--VMCF-FYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIM 247
              || ||  :  ::|: |  | ::     |    | |   |  |||:: : :|:| : |:|:|
Db        209 GFCIPFATILVCYGFIVKALI-----SNDMKTPL-RGKSVRLVIIVLAVFAISYLPFHVM 262

Qy        248 RNLRIASRLDSWPQG---CT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLIS 303
              :|| : |||  : ||   |   : : : | :|| || ||| ::|| ||| || :|
Db        263 KNLNLQSRL--YYQGLDTCEWNRRVYATYQVTRGLASLNSCVDPILYFLAGDTFR----- 315

Qy        304 KFRQYFKSLTSFRT 317
                |::  : : | |
Db        316 --RRFTNAASRFMT 327
```

RESULT 7
Q96P68
ID   Q96P68   PRELIMINARY;   PRT;   337 AA.
AC   Q96P68;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   G protein-coupled receptor GPR99 (Putative G-protein coupled receptor)
DE   (Seven transmembrane helix receptor).
GN   GPR80 OR GPCR OR GPR99.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21458557; PubMed=11574155;
RA   Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
RA   Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT   "Discovery and mapping of ten novel G protein-coupled receptor
RT   genes.";
RL   Gene 275:83-91(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT   "Identification of G protein-coupled receptor genes from the human
RT   genome sequence.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   PubMed=12098360;
RA   Wittenberger T., Hellebrand S., Munck A., Kreienkamp H.J.,
RA   Schaller H.C., Hampe W.;
RT   "GPR99, a new G protein-coupled receptor belonging to a new subgroup
RT   of nucleotide receptors.";
RL   BMC Genomics 3:17-17(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF411109; AAL26480.1; -.
DR   EMBL; AB083598; BAB89311.1; -.
DR   EMBL; AF370886; AAM76912.1; -.
DR   EMBL; AB065877; BAC06095.1; -.
DR   Genew; HGNC:4531; GPR80.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor; Transmembrane.
SQ   SEQUENCE   337 AA; 38251 MW; 6814EA0044756CE6 CRC64;

  Query Match   25.8%; Score 426; DB 4; Length 337;

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  Best Local Similarity   34.4%;  Pred. No. 1.6e-28;
  Matches  101;  Conservative   57;  Mismatches  126;  Indels   10;  Gaps    6;

Qy         17 LNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILI 76
              |  :||   | | |: |  ||  |:  |:| |: | || : : ||: :|  :| :|| ||
Db         31 LKMHYLPVIYGIIFLVGFPGNAVVISTYIFKMRPWKSSTIIMLNLACTDLLYLTSLPFLI 90

Qy         77 KSYAN-DKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA 135
                ||: :   :|| :|   |:  | |||:|||||  |: || :: :|     : |   |
Db         91 HYYASGENWIFGDFMCKFIRFSFHFNLYSSILFLTCFSIFRYCVIIHPMSCFSIHKTRCA 150

Qy        136 ILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLI--YSLCLTLLGFL 193
              ::    || :  : |:||   | |  :   | |:|  ||   | | |  |:| ||   |
Db        151 VVACAVVWIISLVAVIPMTFLITSTNRTNRSACLDLTSS--DELNTIKWYNLILTATTFC 208

Qy        194 IPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIA 253
              :|| ::   |  ::  |    |  :      | :|| :| :: | : | |:||:| :||
Db        209 LPLVIVTLCYTTIIHTLTHGLQTDSCL--KQKARRLTILLLLAFYVCFLPFHILRVIRIE 266

Qy        254 SRLDSWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFR 306
              ||| |    |: :  |   | ::|||| ||:  | : | :: |:::: : |  |
Db        267 SRLLS--ISCSIENQIHEAYIVSRPLAALNTFGNLLLYVVVSDNFQQAVCSTVR 318


RESULT 8
O57466
ID   O57466      PRELIMINARY;      PRT;   374 AA.
AC   O57466;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   G protein coupled P2Y nucleotide receptor.
GN   TP2Y.
OS   Meleagris gallopavo (Common turkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX   NCBI_TaxID=9103;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=98086419; PubMed=9415702;
RA   Boyer J.L., Waldo G.L., Harden T.K.;
RT   "Molecular cloning and expression of an avian G protein-coupled P2Y
RT   receptor.";
RL   Mol. Pharmacol. 52:928-934(1997).
DR   EMBL; AF031897; AAC60339.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   374 AA;  42594 MW;  849C465722BDD02B CRC64;

  Query Match             25.6%;  Score 422.5;  DB 13;  Length 374;
  Best Local Similarity   33.7%;  Pred. No. 3.6e-28;
  Matches  106;  Conservative   59;  Mismatches  119;  Indels   31;  Gaps    8;
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Qy          10 WL------ATEA--ILNKYY----LSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVY 57
               ||       | ||  : |: :    |   | | |: ||  |   :: ::  |: ||::  |
Db          20 WLGGNTTAAAEAKCVFNEEFKFILLPISYGIVFVVGLPLNSWAMWIFVSRMRPWNATTTY 79

Qy          58 LFNLSISDFAFLCTLPILIKSYAN-DKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDR 116
               :|||:|||  :: :|| |:  ||: :   :| | |   |:: : |||:|||||| ||: |
Db          80 MFNLAISDTLYVFSLPTLVYYYADRNNWPFGKVFCKIVRFLFYANLYSSILFLTCISVHR 139

Qy         117 YLLMKYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGN 176
               |: : :| |     | : | || : || :||: ::| | |: :  |:  : | |
Db         140 YMGICHPIRSLKWVKTKHARLICVGVWLVVTICLIPNLIFVTTSSKDNSTLCHDTTKPEE 199

Qy         177 PEHNLIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQ--------- 227
                :| : ||  :  | | ||  |:   |  |   | :||       |   |:
Db         200 FDHYVHYSSSIMALLFGIPFLVIVVCYCLMAKRLCKRS------FPSPSPRVPSYKKRSI 253

Qy         228 RLVVLAVVIFSILFTPYHIMRNLRIASRLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAIN 286
               ::::: : :|:| | |:|| | |   ||   :   | |   |   | :|||||  :|| ::
Db         254 KMIIIVLTVFAICFVPFHITRTLYYTSRY--FQADCQTLNIINFTYKITRPLASINSCLD 311

Qy         287 PIFYFLMGDHYREML 301
               || ||: || ||  |
Db         312 PILYFMAGDKYRGRL 326
```

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RESULT 9
Q8VHP3
ID   Q8VHP3      PRELIMINARY;      PRT;   361 AA.
AC   Q8VHP3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   CC-chemokine receptor 4.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Jopling L.A., Sabroe I., Andrew D.P., Mitchell T.J., Li Y.,
RA   Hodge M.R., Williams T.J., Pease J.E.;
RT   "The identification, characterization and distribution of guinea pig
RT   CCR4 and epitope mapping of a blocking antibody.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF431971; AAL57488.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   361 AA;  41064 MW;  9304E897D4FD6839 CRC64;

  Query Match             21.4%;  Score 353;  DB 11;  Length 361;
  Best Local Similarity   30.0%;  Pred. No. 3e-22;
  Matches   86;  Conservative   62;  Mismatches  131;  Indels    8;  Gaps    5;
```

```
Qy          21 YLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNS-SNVYLFNLSISDFAFLCTLPILIKSY 79
               :|   |:: |:|||||  ||   ||  |   | ::||| ||:|||  |: :||     |
Db          42 FLPPLYSLVFLFGLLGNSVVVL-VLFKYKRLRSMTDVYLLNLAISDLLFVLSLPFW-GYY 99

Qy          80 ANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILIS 139
               | |:  :|  :|    ::      |: | |:  :|:|||| : :       ::   : :: |
Db         100 AADQWVFGLGVCKMISWIYLVGFYSGIFFIVLMSIDRYLAIVHGVFSMRVRTFTYGVITS 159

Qy         140 LAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
               || ||:     || | |     :  ::|    |: :    :: || : :|| :||| :|
Db         160 LATWAVAVFASLPGLLFSTCYTERNHTSCKTRYSANSTTWKVLSSLEINILGLVIPLGIM 219

Qy         200 CFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIASRLDSW 259
                 | | |::    |: |   :   :|  :::   ||:|   :|||:|:  |     |:
Db         220 -LFCYSMII----RTLQHCKSKKKNKAVKMIFAVVVLFLGFWTPYNIVLFLYTLVELEVL 274

Qy         260 PQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFR 306
                    :| :      |  |||::  :||| || :|: :|: ::  |:
Db         275 QDCSLEKYLDFALQATETLAFIHCCLNPIIYFFLGEKFRKYIVQLFK 321
```

```
RESULT 10
Q8MJW8
ID   Q8MJW8      PRELIMINARY;      PRT;   360 AA.
AC   Q8MJW8;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   CC chemokine receptor 4.
GN   CCR4.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Maeda S., Okayama T., Masuda K., Ohno K., Tsujimoto H.;
RT   "Detection of CC chemokine receptor 4 (CCR4) mRNA expression in canine
RT   atopic skin lesion.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB080188; BAC10546.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   360 AA;  41354 MW;  69115F5209EC0908 CRC64;

  Query Match           20.8%;  Score 343;  DB 6;  Length 360;
  Best Local Similarity   29.3%;  Pred. No. 2.2e-21;
  Matches   98;  Conservative   59;  Mismatches  137;  Indels   40;  Gaps   10;

Qy          14 EAILNKYYL-------------SAF--------YAIEFIFGLLGNVTVVFGYLFCMKNWN 52
               |:| | |||              ||        |:: |:|||||| :||   ||  |
Db          13 ESIYNNYYLYENIPKPCTKEGIKAFGELFLPPLYSLVFLFGLLGN-SVVVVVLFKYKRLK 71
```

```
Qy          53 S-SNVYLFNLSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTF 111
               | ::||| ||:|||  |: :||     || |:  :|  ||    ::     |: | |:
Db          72 SMTDVYLLNLAISDLLFVLSLPFW-GYYAADQWVFGLGLCKIISWMYLVGFYSGIFFIML 130

Qy         112 ISMDRYLLMKYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDY 171
               :|:|||| : :       :   : :: ||| |::  |  || | |     :   : |
Db         131 MSIDRYLAIVHAVFSLRARTLTYGVITSLATWSVAVLASLPGLLFSTCYTERNHTYCKTK 190

Qy         172 ASSGNPEHNLIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVV 231
                | :    :: || : :|| :|||  |  | | |::    |: |         |  |:|
Db         191 YSRNSTRWKVLSSLEINILGLVIPLGTM-LFCYSMII----RTLQHCKNEKKSKAVRMVF 245

Qy         232 LAVVIFSILFTPYHIMRNLRIASRLDSWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFY 290
              | :|   : ||::: |     |:   | || :: :      |  |||::  :||: |
Db         246 AVVALFLGFWAPYNVVLFLETLVELEVL-QDCTFERHLDYAIQATETLAFVHCCLNPVIY 304

Qy         291 FLMGDHYREMLISKFR---------QYFKSLTSF 315
               | :|: :|: |:  |:          || : |  :
Db         305 FFLGEKFRKYLVQLFKTCRGPFMLCQYCRLLQMY 338
```

```
RESULT 11
Q9ERK9
ID   Q9ERK9      PRELIMINARY;      PRT;   328 AA.
AC   Q9ERK9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   P2Y6 receptor (Hypothetical 36.7 kDa protein).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvEv;
RX   MEDLINE=21160052; PubMed=11259526;
RA   Lazarowski E.R., Rochelle L.G., O'Neal W.K., Ribeiro C.M.P.,
RA   Grubb B.R., Zhang V., Harden T.K., Boucher R.C.;
RT   "Cloning and functional characterization of two murine uridine
RT   nucleotide receptors reveal a potential target for correcting ion
RT   transport deficiency in cystic fibrosis gallbladder.";
RL   J. Pharmacol. Exp. Ther. 297:43-49(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF298899; AAG24619.1; -.
DR   EMBL; BC027331; AAH27331.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Hypothetical protein; Receptor.
SQ   SEQUENCE   328 AA;  36721 MW;  00F9DF5ADADF903E CRC64;
```

```
  Query Match             20.5%;  Score 338;  DB 11;  Length 328;
  Best Local Similarity   29.6%;  Pred. No. 5.3e-21;
  Matches   84;  Conservative   54;  Mismatches  136;  Indels   10;  Gaps    4;

Qy         22 LSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSYA- 80
              |:  |::  : ||  |: |:       :    | ||  ||:::|  : |:||:|| :||
Db         29 LTPVYSVVLVVGLPLNICVIAQICASRRTLTRSAVYTLNLALADLMYACSLPLLIYNYAR 88

Qy         81 NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFRE-HFLQKKEFAILIS 139
               |   :||: |   |:: : ||: ||||||  ||  ||| : :|    |    :  | ::
Db         89 GDHWPFGDLACRFVRFLFYANLHGSILFLTCISFQRYLGICHPLASWHKRGGRRAAWVVC 148

Qy        140 LAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
              ||  || : ||   |  :  :   : | | :        | | : ||::|||:|   :
Db        149 GVVWLAVTAQCLPTAVFAATGIQRNRTVCYDLSPPILSTRYLPYGMALTVIGFLLPFIAL 208

Qy        200 CFFYYKMVVFLKRRSQQQATALPL-----DKPQRLVVLAVVIFSILFTPYHIMRNLRIAS 254
                | :|   :|  :|   | |:      |  |: |:   :|:| | |:|| :   :|
Db        209 LACYCRMA---RRLCRQDGPAGPVAQERRSKAARMAVVVAAVFAISFLPFHITKTAYLAV 265

Qy        255 RLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYR 298
              |          :   : |  ||| | :|| ::|| ::     :|
Db        266 RSTPGVSCPVLETFAAAYKGTRPFASVNSVLDPILFYFTQQKFR 309


RESULT 12
Q9MYJ8
ID   Q9MYJ8      PRELIMINARY;      PRT;   355 AA.
AC   Q9MYJ8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Chemokine receptor.
GN   CCR1.
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX   NCBI_TaxID=9483;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20153429; PubMed=10686294;
RA   Liang M., Rosser M.P., Ng H.P., May K., Bauman J.G., Islam I.,
RA   Ghannam A., Kretschmer P.J., Pu H., Dunning L., Snider R.M.,
RA   Morrissey M.M., Hesselgesser J., Perez H.D., Horuk R.;
RT   "Species selectivity of a small molecule antagonist for the CCR1
RT   chemokine receptor.";
RL   Eur. J. Pharmacol. 389:41-49(2000).
DR   EMBL; AF127528; AAF36453.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   355 AA;  40928 MW;  2B01C47E9874A2C1 CRC64;

  Query Match             20.3%;  Score 335;  DB 6;  Length 355;
```

```
  Best Local Similarity   28.1%;  Pred. No. 1e-20;
  Matches   85;  Conservative   63;  Mismatches  138;  Indels   16;  Gaps    7;

Qy         12 ATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCT 71
              | |       |   |:: |: ||:||: ||   :   :  | :::|| ||:|||  || |
Db         27 ANERAFGAKLLPPLYSLVFVIGLVGNILVVVVLVQYKRLKNMTSIYLLNLAISDLLFLFT 86

Qy         72 LPILIKSYANDKGTYGDVLC--ISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFL 129
              ||  |         :|: :|  :|  |  :| ||: | |:  :::|||| : :
Db         87 LPFWISYQLKTDWVFGNAMCKVLSGFY--YTGLYSEIFFIILLTIDRYLAIVHAVFALRA 144

Qy        130 QKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNC-IDYASSGNPEHNLIYSLCLT 188
              :   | :: |: :| |  |  || | |  :  :     | : :       |  |  :| |
Db        145 RTVTFGVITSIIIWVLAILASLPGLYFAKTQWEITHRTCSLHFPHESRQEWKLFQALKLN 204

Qy        189 LLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMR 248
              ||| ::|| ||   |  ::  | ||  :: :     |  ||: : ::|| : :|||::
Db        205 LLGLVLPLLVMIVCYTGIIKILLRRPNEKKS-----KAVRLIFVIMIIFFLFWTPYNLTT 259

Qy        249 NLRIASRLDSWPQGCTQ-KAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQ 307
               : :      :  || | : :     :|  :|: :  :||: |  :|: :|: |    ||
Db        260 LISVFQDF-LFTYGCEQGRQLDLAIQVTEMIAYTHCCVNPVIYAFVGERFRKHL----RQ 314

Qy        308 YF 309
              |
Db        315 LF 316


RESULT 13
Q9JLY8
ID   Q9JLY8      PRELIMINARY;      PRT;   355 AA.
AC   Q9JLY8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Macrophage inflammatory protein-1 alpha receptor.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CD;
RX   MEDLINE=20555330; PubMed=11091494;
RA   Waller A., Nayee P., Czaplewski L.G.;
RT   "Identification and characterization of a rat macrophage inflammatory
RT   protein-1 alpha receptor.";
RL   J. Hematother. Stem Cell Res. 9:703-710(2000).
DR   EMBL; AF119381; AAF34340.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   355 AA;  40838 MW;  2FEB8661D1E6E075 CRC64;
```

```
  Query Match             20.2%;  Score 333;  DB 11;  Length 355;
  Best Local Similarity   28.6%;  Pred. No. 1.5e-20;
  Matches   85;  Conservative   69;  Mismatches  119;  Indels   24;  Gaps    9;

Qy         22 LSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSYAN 81
              |   |:  || |::||: |:   :   :  : :::|||||::||  || |||  |
Db         37 LPPLYSFVFIIGVVGNILVILVLMQHRRLQSMTSIYLFNLAVSDLVFLFTLPFWIDYKLK 96

Qy         82 DKGTYGDVLC--ISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILIS 139
              |   :|| :|  :|  | |   ||: | |:  :::|||| : :       :   | |: |
Db         97 DNWVFGDAMCKLLSGFYYL--GLYSEIFFIILLTIDRYLAIVHAVFSLRARTVTFGIITS 154

Qy        140 LAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNL-----IYSLCLTLLGFLI 194
              : :|||  |  :| | |  :  :     |    |   |: :|       :| | ||| ::
Db        155 IIIWALAILASIPALCFFKAQWEFTHHTC----SPHFPDESLKTWKRFQALKLNLLGLIL 210

Qy        195 PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIA 253
              || ||   |  :: : |:| ::::| |:      ||:    ::| :|:|||::   : ::
Db        211 PLLVMIICYAGIIRILLRRPNEKKAKAV------RLIFAITLLFFLLWTPYNL--TVFVS 262

Qy        254 SRLD-SWPQGCTQ-KAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQY 308
              :  |  :   | | | :     :|  :|: :  :||| |  :|: :|: |   |:::
Db        263 AFQDVLFTNQCEQSKQLDLAIQVTEVIAYTHCCVNPIIYVFVGERFRKYLRQLFQRH 319


RESULT 14
Q8CBJ0
ID   Q8CBJ0      PRELIMINARY;      PRT;   354 AA.
AC   Q8CBJ0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Chemokine.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK035902; BAC29236.1; -.
SQ   SEQUENCE   354 AA;  40232 MW;  F2294B080D75BCA3 CRC64;

  Query Match             19.8%;  Score 326.5;  DB 11;  Length 354;
  Best Local Similarity   28.2%;  Pred. No. 5.5e-20;
  Matches   82;  Conservative   59;  Mismatches  133;  Indels   17;  Gaps    5;

Qy         21 YLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSYA 80
              :|| |||: | |||:||: ||       |  : :::|| ||::||  |: |||
Db         34 FLSVFYALVFTFGLVGNLLVVLALTNSRKPKSITDIYLLNLALSDLLFVATLPFWTHYLI 93
```

```
Qy          81 NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILISL 140
               : :| : : :|           :  | |:| ||:|||| :         :  :  : |||
Db          94 SHEGLH-NAMCKLTTAFFFIGFFGGIFFITVISIDRYLAIVLAANSMNNRTVQHGVTISL 152

Qy         141 AVWALVTLEVLPMLTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
                |||   |   |   |     | : : |: ||         :: :  : :||| :|| .|
Db         153 GVWAAAILVASPQFMF----TKRKDNECLGDYPEVLQEMWPVLRNSEVNILGFALPLLIM 208

Qy         200 CFFYYKMVVFL---KRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
                | |:::: |   | | : :|          ||::| |  | : :|||:||  |
Db         209 SFCYFRIIQTLFSCKNRKKARAV--------RLILLVVFAFFLFWTPYNIMIFLETLKLY 260

Qy         257 DSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQ 307
               : :|    :: ::   ::|  :|| :  :||  |   |: :|  |   :|:
Db         261 NFFPSCDMKRDLRLALSVTETVAFSHCCLNPFIYAFAGEKFRRYLGHLYRK 311
```

RESULT 15
Q9MYJ9
ID   Q9MYJ9   PRELIMINARY;   PRT;   351 AA.
AC   Q9MYJ9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Chemokine receptor.
GN   CCR1.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20153429; PubMed=10636294;
RA   Liang M., Rosser M.P., Ng H.P., May K., Bauman J.G., Islam I.,
RA   Ghannam A., Kretschmer P.J., Pu H., Dunning L., Snider R.M.,
RA   Morrissey M.M., Hesselgesser J., Perez H.D., Horuk R.;
RT   "Species selectivity of a small molecule antagonist for the CCR1
RT   chemokine receptor.";
RL   Eur. J. Pharmacol. 389:41-49(2000).
DR   EMBL; AF127527; AAF36452.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   351 AA; 40534 MW; B3FED6117A141552 CRC64;

  Query Match   19.8%; Score 326; DB 6; Length 351;
  Best Local Similarity   27.8%; Pred. No. 6e-20;
  Matches   83; Conservative   65; Mismatches 137; Indels   14; Gaps   7;

```
Qy          22 LSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSYAN 81
                  |   |:: |: ||:||| ||   :   : : :::|| ||:|||  || |||  |
Db          37 LPPLYSLVFVIGLVGNVLVVLVLMKYKRLRSMTSIYLLNLAISDLLFLFTLPFWIDYRLK 96

Qy          82 DKGTYGDVLC--ISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILIS 139
```

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                |   :|||||  :|  |  :  ||: : |:  :::|||| : :       :   | |: |
Db          97 DDWVFGDVLCKFLSGLY--YVGLYSEVFFIILLTIDRYLAIVHAVFALRARTVSFGIVTS 154

Qy         140 LAVWALVTLEVLPMLTFINSVPKEEGSNC-IDYASSGNPEHNLIYSLCLTLLGFLIPLSV 198
               :  |||  |  :|   |  :  :     | : :      :     :| | :|| ::|| |
Db         155 IVTWALTILAAIPGFRFSKTQWEFTHYTCSLHFPHESLRQWKQFQALKLNILGLVLPLLV 214

Qy         199 MCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIASRLDS 258
               |   |  ::  | ||  :: :     :  ||: : ::|| : :|||::   | :::  ||
Db         215 MVVCYTGIIQILLRRPNEKKS-----RAVRLIFVIMLIFFLFWTPYNL--TLLVSAFQDS 267

Qy         259 -WPQGCTQ-KAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSLTSF 315
                :   | | | :     :|  :|: :  :||: |  :|: ::: |   |  |      |
Db         268 LFTNQCEQSKQLDLAIQVTEVIAYTHCCVNPVIYVFVGERFQKYLRQLFHTYLAKWLPF 326
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Search completed: December 12, 2003, 18:08:32
Job time : 41 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 12, 2003, 17:58:12 ; Search time 40 Seconds
(without alignments)
1257.908 Million cell updates/sec

Title: US-09-891-138A-2
Perfect score: 1650
Sequence: 1 MAQNLSCENWLATEAILNKY.....REMLISKFRQYFKSLTSFRT 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1650	100.0	317	23	AAU74904	Amino acid sequenc
2	1238.5	75.1	330	24	ABP81696	Human purinergic r
3	1238.5	75.1	334	21	AAY71308	Human orphan G pro
4	1238.5	75.1	334	21	AAB02842	Human G protein co
5	1238.5	75.1	334	23	ABB90381	Human polypeptide
6	1238.5	75.1	371	24	ABR41222	Human DITHP recept
7	1238.5	75.1	379	23	AAE15633	Human G-protein co
8	1231.5	74.6	334	24	ABG72131	Human adenosine re
9	1226.5	74.3	334	18	AAW19854	Human purinergic r
10	1219.5	73.9	334	18	AAW22732	Human ATP receptor
11	1216.5	73.7	387	22	AAU31029	Novel human secret
12	1014.5	61.5	258	21	AAB45376	Human secreted pro
13	479	29.0	373	23	ABP54317	Rat P2Y purinocept
14	479	29.0	373	24	ABU11903	Rat purinergic rec
15	474	28.7	373	22	AAE04389	Human P2-purinergi
16	474	28.7	373	23	ABP54315	Bovine P2Y purinoc
17	474	28.7	373	23	ABP54316	Human P2Y purinoce
18	474	28.7	373	23	AAU10983	Purinergic recepto
19	474	28.7	373	23	AAU10984	Purinergic recepto
20	474	28.7	373	24	ABP81867	Human purinergic r
21	472.5	28.6	362	23	ABP54313	Chicken P2Y purino
22	472.5	28.6	362	23	ABP54314	Turkey P2Y purinoc
23	472.5	28.6	362	24	ABU11901	Chicken purinergic
24	472.5	28.6	362	24	ABU11902	Turkey purinergic
25	467	28.3	373	23	AAU10985	Purinergic recepto
26	426	25.8	337	22	AAU04375	Human G-protein co
27	426	25.8	337	23	ABP95602	Human GPCR polypep
28	426	25.8	337	23	ABG70271	Human Purinoceptor
29	426	25.8	337	23	ABG76871	Human G-protein co
30	426	25.8	337	23	ABG70287	Human novel polype
31	426	25.8	337	23	AAO15399	Human G protein-co
32	426	25.8	337	23	ABB81902	Human G-protein co
33	426	25.8	337	23	ABB83819	Human P2Y-like rec
34	426	25.8	337	23	AAE21803	Human AXOR89 (G-pr
35	426	25.8	337	23	ABB79438	Human P2Y1-li. Ho
36	426	25.8	337	23	AAU77600	Human P2Y1-like G
37	426	25.8	337	23	AAO14027	Human purinergic-r
38	426	25.8	337	23	AAE16171	Human G-protein co
39	426	25.8	337	24	ABP71377	Human TGR164 prote
40	426	25.8	338	24	AAE33315	Human TARZAN prote
41	426	25.8	345	24	AAE33318	Human TARZAN prote
42	426	25.8	363	24	AAE33317	Human TARZAN prote
43	422.5	25.6	374	22	AAE04390	Turkey P2Y nucleot
44	419	25.4	337	22	AAU04584	Human G-protein co
45	419	25.4	337	24	ABP81736	Human G protein-co

ALIGNMENTS

RESULT 1
AAU74904
ID AAU74904 standard; Protein; 317 AA.
XX
AC AAU74904;
XX
DT 09-APR-2002 (first entry)
XX
DE Amino acid sequence of mouse G-protein coupled receptor TGR18 protein.
XX
KW Mouse; G-protein coupled; receptor; GPCR; TGR18; kidney disease;
KW signal transduction modulator; cerebral cavernous malformation;
KW hyperlipidemia; obesity; dyslexia; cardiac myxoma; renal failure;
KW nephritis; hypertension; liver disease; cirrhosis; blood disorder;
KW spleen-associated disorder; immune disorder.
XX
OS Mus sp.
XX
PN WO200200719-A2.
XX
PD 03-JAN-2002.
XX
PF 25-JUN-2001; 2001WO-US20363.
XX
PR 23-JUN-2000; 2000US-213461P.
XX
PA (TULA-) TULARIK INC.
XX
PI Lin DC, Zhao J, Chen J, Cutler G;
XX
DR WPI; 2002-147880/19.
DR N-PSDB; ABK12957.
XX
PT New G-protein coupled receptor polypeptides, useful for identifying
PT modulators of signal transduction for treating kidney disease,
PT hyperlipidemia, obesity, dyslexia and cardiac myxoma
XX
PS Claim 33; Page 59; 78pp; English.
XX
CC The present invention relates to a new G-protein coupled receptor (GPCR)
CC polypeptide comprising greater than 70% amino acid sequence identity to
CC the amino acid sequence of human GPCRs TGR62, TGR21, TGR130.1, TGR130.2,
CC human TGR213 or TGR92, 80% amino acid sequence identity to mouse TGR18
CC or 90% amino acid sequence identity to human novel edg receptor protein,
CC as defined in the specification. The GPCR covalently linked to a solid
CC phase is useful for identifying a compound that modulates signal
CC transduction. The identified compounds are useful for treating
CC kidney disease, cerebral cavernous malformations, hyperlipidemia,
CC obesity, dyslexia and cardiac myxoma. The molecules of the invention are
CC useful for diagnosing disorders or conditions such as kidney-related
CC conditions or diseases such as renal failure, nephritis, nephrotic
CC syndrome, asymptomatic urinary abnormalities, renal tubule defects,
CC hypertension and nephrolithiasis, liver-related disease or condition
CC e.g. cirrhosis, infiltrations, lesions, functional disorders and jaundice
CC and spleen-associated disorders or conditions e.g. splenic enlargement,
CC immune disorders, blood disorders and others. Modulation of the
CC polypeptide of the invention is useful to treat or prevent any of the

CC above conditions or diseases. The present amino acid sequence represents
CC the mouse GPCR TGR18 protein of the invention. This sequence is one of
CC seven novel G protein coupled receptors of the invention (AAU74904-
CC AAU74911).
XX
SQ Sequence 317 AA;

Query Match 100.0%; Score 1650; DB 23; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.3e-157;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240

Qy        241 FTPYHIMRNLRIASRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 FTPYHIMRNLRIASRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREM 300

Qy        301 LISKFRQYFKSLTSFRT 317
              |||||||||||||||||
Db        301 LISKFRQYFKSLTSFRT 317
```

RESULT 2
ABP81696
ID ABP81696 standard; Protein; 330 AA.
XX
AC ABP81696;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human purinergic receptor P2U2 protein SEQ ID NO:567.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US50107.
XX
PR 19-DEC-2000; 2000US-257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
DR N-PSDB; ABZ42542.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases -
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity
CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
CC an antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention.
XX
SQ Sequence 330 AA;

Query Match 75.1%; Score 1238.5; DB 24; Length 330;
Best Local Similarity 72.2%; Pred. No. 3.7e-116;
Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

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Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              || | :|:|||| || | ||||| || |||: |:||| ||:||:| :|||||||:||||
Db          1 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 60

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:||||    |||||||||||||| ||||||||||||:||||::
Db         61 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 120

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||| |||||||||||||:| |||||:||:|  || |  : |: | |:||||:| :|
Db        121 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 180

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||:|||||||||||| |||||||: :|||:|::| ||||||:||  ||::||||||:|
Db        181 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 240

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:|||||| || |  |||  | | | :|||||||| |||:||||:|||:|:
Db        241 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 300

Qy        300 MLISKFRQYFKSLTSF 315
              ||::: |  |||||||
Db        301 MLMNQLRHNFKSLTSF 316
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RESULT 3
AAY71308
ID   AAY71308 standard; Protein; 334 AA.
XX
AC   AAY71308;
XX
DT   02-NOV-2000 (first entry)
XX
DE   Human orphan G protein-coupled receptor hCHN10.
XX
KW   Human; orphan G protein-coupled receptor; GPCR; hCHN10; drug screening;
KW   transmembrane receptor; expressed sequence tag; EST; signal cascade.
XX
OS   Homo sapiens.
XX
PN   WO200031258-A2.
XX
PD   02-JUN-2000.
XX
PF   13-OCT-1999;   99WO-US23687.
XX
PR   20-NOV-1998;   98US-0109213.
PR   16-FEB-1999;   99US-0120416.
PR   26-FEB-1999;   99US-0121852.
PR   12-MAR-1999;   99US-0123946.
PR   12-MAR-1999;   99US-0123949.
PR   26-MAY-1999;   99US-0136436.
PR   26-MAY-1999;   99US-0136437.
PR   28-MAY-1999;   99US-0136439.
PR   26-MAY-1999;   99US-0136567.
PR   28-MAY-1999;   99US-0137127.
PR   28-MAY-1999;   99US-0137131.

PR 29-JUN-1999; 99US-0141448.
PR 29-SEP-1999; 99US-0156555.
PR 29-SEP-1999; 99US-0156633.
PR 29-SEP-1999; 99US-0156634.
PR 29-SEP-1999; 99US-0156653.
PR 01-OCT-1999; 99US-0157280.
PR 01-OCT-1999; 99US-0157281.
PR 01-OCT-1999; 99US-0157282.
PR 01-OCT-1999; 99US-0157293.
PR 01-OCT-1999; 99US-0157294.
PR 12-OCT-1999; 99US-0416760.
PR 12-OCT-1999; 99US-0417044.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Chen R, Dang HT, Liaw CW, Lin I;
XX
DR WPI; 2000-400068/34.
DR N-PSDB; AAD01135.
XX
PT Novel human orphan G protein-coupled receptors and the encoding cDNAs
PT for use in the identification of G protein-coupled receptor agonists -
XX
PS Claim 70; Page 87-88; 102pp; English.
XX
CC The present amino acid sequence is the hCHN10, an endogenous human
CC orphan G protein-coupled receptor (GPCR), expressed in kidney and
CC thyroid. The hCHN10 cDNA was identified using the human EST (expressed
CC sequence tag) 1365839 as a probe. The orphan GPCR of the invention, like
CC all GPCRs has seven transmembrane alpha helices with an extracellular
CC N-terminus and an intracellular C-terminus. However, no endogenous
CC ligands has yet been identified for the proteins of the invention. The
CC orphan GPCRs may be used in the identification of their endogenous
CC ligands, and to screen potential GPCR agonists and antagonists for use as
CC pharmaceutical agents. The proteins may also be used in the study of
CC GPCR-mediated signalling cascades, and to elucidate their precise role in
CC normal and diseased human conditions. Nucleic acid encoding human orphan
CC GPCRs may be used for tissue localisation expression analysis to provide
CC information about their function in healthy and pathological states.
XX
SQ Sequence 334 AA;

Query Match 75.1%; Score 1238.5; DB 21; Length 334;
Best Local Similarity 72.2%; Pred. No. 3.8e-116;
Matches 238; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

```
Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              ||  | :|:|||| ||  | ||||| ||  |||: |:|||  ||:||:| :|||||||:||||
Db          5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:|||    |||||||||||||| ||||||||||||:||||::
Db         65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||| |||||||||||||:| |||||:||:|  || |  : |: | |:||||:| :|
Db        125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184
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```
Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||:|||||||||||| |||||||: :|||:|::| ||||||:||  ||::||||||:|
Db        185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 244

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:|||||| || |  |||  | | | :||||||||| |||:||||:|||:|:
Db        245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304

Qy        300 MLISKFRQYFKSLTSF 315
              ||::: |  |||||||
Db        305 MLMNQLRHNFKSLTSF 320
```

RESULT 4
AAB02842
ID AAB02842 standard; Protein; 334 AA.
XX
AC AAB02842;
XX
DT 22-AUG-2000 (first entry)
XX
DE Human G protein coupled receptor hCHN10 protein SEQ ID NO:38.
XX
KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical;
KW mutant.
XX
OS Homo sapiens.
XX
PN WO200022131-A2.
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99WO-US24065.
XX
PR 13-OCT-1998; 98US-0170496.
PR 12-NOV-1998; 98US-0108029.
PR 20-NOV-1998; 98US-0109213.
PR 27-NOV-1998; 98US-0110060.
PR 16-FEB-1999; 99US-0120416.
PR 26-FEB-1999; 99US-0121852.
PR 12-MAR-1999; 99US-0123944.
PR 12-MAR-1999; 99US-0123945.
PR 12-MAR-1999; 99US-0123946.
PR 12-MAR-1999; 99US-0123948.
PR 12-MAR-1999; 99US-0123949.
PR 12-MAR-1999; 99US-0123951.
PR 28-MAY-1999; 99US-0136436.
PR 28-MAY-1999; 99US-0136437.
PR 28-MAY-1999; 99US-0136439.
PR 28-MAY-1999; 99US-0137127.
PR 28-MAY-1999; 99US-0137131.
PR 28-MAY-1999; 99US-0137567.
PR 30-JUN-1999; 99US-0141448.
PR 27-AUG-1999; 99US-0151114.
PR 03-SEP-1999; 99US-0152524.

PR 29-SEP-1999; 99US-0156633.
PR 29-SEP-1999; 99US-0156555.
PR 29-SEP-1999; 99US-0156634.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX
DR WPI; 2000-317986/27.
DR N-PSDB; AAA46036.
XX
PT Non-endogenous, human G protein-coupled receptors for screening
PT receptor, inverse or partial agonists useful as therapeutic agents -
XX
PS Example 1; Page 117-118; 187pp; English.
XX
CC The present invention describes transmembrane receptors, preferably
CC human G protein coupled receptors (GPCR), for which the endogenous
CC ligand is unknown (orphan GPCR receptors). More specifically the present
CC invention relates to non-endogenous, constitutively activated versions
CC of a human GPCR. These non-endogenous human GPCRs can be useful for
CC the direct identification of candidate compounds as receptors agonists,
CC inverse agonists or partial agonists for use as pharmaceutical agents.
CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
CC the exemplification of the present invention.
XX
SQ Sequence 334 AA;

Query Match 75.1%; Score 1238.5; DB 21; Length 334;
Best Local Similarity 72.2%; Pred. No. 3.8e-116;
Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

```
Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              || | :|:|||| || | ||||| || |||: |:||| ||:||:| :|||||||:||||
Db          5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:|||| |||||||||||||| ||||||||||||:||||::
Db         65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||| |||||||||||||:| |||||:||:|  || |  : |: | |:||||:| :|
Db        125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||:|||||||||| |||||||: :|||:|::| ||||||:||  ||::||||||:|
Db        185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 244

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:|||||| || |  |||  | | | :||||||||| |||:||||:|||:|:
Db        245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304

Qy        300 MLISKFRQYFKSLTSF 315
              ||::: |  |||||||
Db        305 MLMNQLRHNFKSLTSF 320
```

RESULT 5
ABB90381
ID ABB90381 standard; Protein; 334 AA.
XX
AC ABB90381;
XX
DT 24-MAY-2002 (first entry)
XX
DE Human polypeptide SEQ ID NO 2757.
XX
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection; human; secreted protein.
XX
OS Homo sapiens.
XX
PN WO200190304-A2.
XX
PD 29-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-US16450.
XX
PR 19-MAY-2000; 2000US-205515P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-122018/16.
DR N-PSDB; ABL90790.
XX
PT Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
PT prevention of neural, immune system, muscular, reproductive,
PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
PT disorders -
XX
PS Claim 11; SEQ ID NO 2757; 2081pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (ABL89449-ABL90853) and proteins
CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 334 AA;

Query Match 75.1%; Score 1238.5; DB 23; Length 334;
Best Local Similarity 72.2%; Pred. No. 3.8e-116;
Matches 228; Conservative 42; Mismatches 45; Indels 1; Gaps 1;

```
Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              || | :|:|||| || | ||||| || |||: |:|||  ||:||:| :|||||||:||||
Db          5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:||||    |||||||||||||| ||||||||||||:||||::
Db         65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||| |||||||||||||:| |||||:||:|  || |  : |: | |:||||:| :|
Db        125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||:|||||||||| |||||||| :|||:|::| |||||:|| ||::|||||:|
Db        185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 244

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:|||||| || |  ||| | | | :|||||||| |||:||||:|||:|:
Db        245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304

Qy        300 MLISKFRQYFKSLTSF 315
              ||:::| |||||||
Db        305 MLMNQLRHNFKSLTSF 320
```

RESULT 6
ABR41222
ID ABR41222 standard; Protein; 371 AA.
XX
AC ABR41222;
XX
DT 02-JUN-2003 (first entry)
XX
DE Human DITHP receptor.
XX
KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
KW cancer; cell proliferative disorder; autoimmune disorder;
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
KW neurological disorder; gastrointestinal disorder; transport disorder;
KW connective tissue disorder; drug screening; proteome analysis;
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
KW disease model; toxicological testing; transcript imaging;
KW receptor.
XX
OS Homo sapiens.
XX
PN WO200297031-A2.
XX

PD 05-DEC-2002.
XX
PF 27-MAR-2002; 2002WO-US10056.
XX
PR 28-MAR-2001; 2001US-279619P.
PR 29-MAR-2001; 2001US-280067P.
PR 29-MAR-2001; 2001US-280068P.
PR 16-MAY-2001; 2001US-291280P.
PR 17-MAY-2001; 2001US-291829P.
PR 17-MAY-2001; 2001US-291849P.
PR 19-JUN-2001; 2001US-299428P.
PR 20-JUN-2001; 2001US-299776P.
PR 20-JUN-2001; 2001US-300001P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
DR WPI; 2003-129518/12.
DR N-PSDB; ACC46165.
XX
PT Novel human diagnostic and therapeutic polypeptide useful for
PT identifying test compound which specifically binds to a polypeptide
PT encoded by human diagnostic and therapeutic polynucleotide, and to
PT induce antibodies -
XX
PS Claim 27; SEQ ID No 757; 591pp; English.
XX
CC The invention relates to novel human diagnostic and therapeutic
CC polynucleotides designated dithp (ACC46080-ACC46749) and to their
CC encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates
CC to polynucleotide sequences at least 90% identical to the dithp cDNA
CC sequences of the invention; recombinant vectors, host cells and
CC transgenic organisms comprising a dithp nucleic acid sequence; the
CC recombinant production of DITHP proteins; antibodies specific for DITHP
CC proteins; microarrays comprising dithp nucleic acid sequences; methods
CC of detecting dithp nucleotide and protein sequences; methods of screening
CC for compounds which specifically bind a DITHP protein; and methods of
CC assessing the toxicity of test compounds using a dithp hybridisation
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
CC diagnosis of a wide variety of conditions including cancer and other cell
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
CC viral, fungal or parasitic infections; hormonal disorders; metabolic
CC disorders; neurological disorders; gastrointestinal disorders; transport
CC disorders; and connective tissue disorders. They may also be used to
CC screen for modulators of protein activity or gene expression. DITHP
CC proteins can additionally be used in analysis of the proteome of a tissue
CC or cell type and to induce antibodies. The dithp nucleic acids are
CC additionally useful in somatic or germline gene therapy of the disorders
CC mentioned above, as a source of antisense sequences, as a source of
CC probes and primers, in genotyping and identification of individuals, in
CC the generation of transgenic animal models of human disease or knock in
CC humanised animals, in toxicological testing, and in transcript imaging.

```
CC   The present sequence represents a DITHP protein which has receptor
CC   activity.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   371 AA;

  Query Match             75.1%;  Score 1238.5;  DB 24;  Length 371;
  Best Local Similarity   72.2%;  Pred. No. 4.4e-116;
  Matches  228;  Conservative   42;  Mismatches   45;  Indels    1;  Gaps    1;

Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              || | :|:|||| || | ||||| || |||: |:||| ||:||:| :|||||||:||||
Db         42 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 101

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:||||    |||||||||||||| ||||||||||||:||||::
Db        102 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 161

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||| |||||||||||||:| |||||:||:|  || |  : |: | |:||||:| :|
Db        162 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 221

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||:|||||||||| |||||||: :|||:|::| ||||||:||  ||::||||||:|
Db        222 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 281

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFFLMGDHYRE 299
              |||||:|||:|||||| || |  |||  | | | :||||||||| |||:||||:|||:|:
Db        282 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 341

Qy        300 MLISKFRQYFKSLTSF 315
              ||::: |  |||||||
Db        342 MLMNQLRHNFKSLTSF 357


RESULT 7
AAE15633
ID   AAE15633 standard; Protein; 379 AA.
XX
AC   AAE15633;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Human G-protein coupled receptor-3 (GCREC-3) protein.
XX
KW   Human; G-protein coupled receptor-3; GCREC-3; therapy; cancer; stroke;
KW   cell proliferative disorder; neurological; epilepsy; Parkinson's disease;
KW   Alzheimer's disease; inflammation; thyroiditis; haemolytic anaemia; AIDS;
KW   Acquired Immune Deficiency Syndrome; dementia; nootropic; cholelithiasis;
KW   multiple sclerosis; atherosclerosis; angina pectoris; gastroenteritis;
KW   diabetes; ulcer; viral infection; immunosuppressive.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
```

FT Domain 187..206
FT /label= Transmembrane_domain
FT Domain 234..253
FT /label= Transmembrane_domain
FT Domain 276..296
FT /label= Transmembrane_domain
FT Domain 319..342
FT /label= Transmembrane_domain
XX
PN WO200198351-A2.
XX
PD 27-DEC-2001.
XX
PF 15-JUN-2001; 2001WO-US19275.
XX
PR 16-JUN-2000; 2000US-212483P.
PR 22-JUN-2000; 2000US-213954P.
PR 29-JUN-2000; 2000US-215209P.
PR 07-JUL-2000; 2000US-216595P.
PR 14-JUL-2000; 2000US-218936P.
PR 19-JUL-2000; 2000US-219154P.
PR 21-JUL-2000; 2000US-220141P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Baughn MR, Hafalia AJA, Nguyen DB, Gandhi AR, Kallick DA;
PI Griffin JA, Yue H, Khan FA, Patterson C, Lu DAM, Tribouley CM;
PI Lu Y, Walia NK, Graul R, Yao MG, Yang J, Ramkumar J, Au-Young J;
PI Elliott VS, Hernandez R, Walsh RT, Borowsky ML, Thornton M, He A;
XX
DR WPI; 2002-075627/10.
DR N-PSDB; AAD24958.
XX
PT Isolated human G-protein coupled receptor polypeptides and the use of
PT these sequences in the diagnosis, treatment and prevention of diseases
PT and in the assessment of exogenous compounds on the expression of the
PT receptors -
XX
PS Claim 1; Page 115-116; 143pp; English.
XX
CC The invention relates to isolated human G-protein coupled receptor
CC (GCREC) polypeptides and their biologically active fragments. GCREC and
CC protein is useful in treating a disease or condition associated with an
CC increase or decrease in expression of functional GCREC. The GCREC's are
CC useful in the diagnosis, treatment and prevention of cell proliferative
CC disorders (cancer, leukaemia, melanoma); neurological disorders (stroke,
CC epilepsy, Parkinson's disease, dementia, Alzheimer's disease); autoimmune
CC inflammatory disorder (thyroiditis, haemolytic anaemia, AIDS, multiple
CC sclerosis); cardiovascular disorder (atherosclerosis, angina pectoris),
CC gastrointestinal disorder (ulcer, cholelithiasis, gastroenteritis),
CC metabolic disorders (diabetes); viral infections (herpes virus) and in
CC the assessment of the effects of exogenous compounds on the expression
CC of the nucleic acid and amino acid sequences. The present sequence is
CC human GCREC-3 protein.
XX
SQ Sequence 379 AA;

```
  Query Match             75.1%;  Score 1238.5;  DB 23;  Length 379;
  Best Local Similarity   72.2%;  Pred. No. 4.5e-116;
  Matches  228;  Conservative   42;  Mismatches   45;  Indels    1;  Gaps    1;

Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              || | :|:|||| || | ||||| || |||: |:||| ||:||:| :|||||||:||||
Db         50 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 109

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:|||| ||||||||||||| ||||||||||||:||||::
Db        110 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 169

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||| |||||||||||||:| |||||:||:|  || |  : |: | |:||||:| :|
Db        170 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 229

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||:|||||||||| |||||||: :|||:|::| ||||||:||  ||::|||||||:|
Db        230 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 289

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:|||||| || |  |||  | | | :||||||||| |||:||||:|||:|:
Db        290 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 349

Qy        300 MLISKFRQYFKSLTSF 315
              ||::: |  |||||||
Db        350 MLMNQLRHNFKSLTSF 365
```

```
RESULT 8
ABG72131
ID   ABG72131 standard; Protein; 334 AA.
XX
AC   ABG72131;
XX
DT   30-JAN-2003  (first entry)
XX
DE   Human adenosine receptor.
XX
KW   Human; mammalian; adenosine receptor; G-protein coupled receptor;
KW   GPCR; adenosine-mediated medical condition; vasodilation; hypotension;
KW   reversal of tachycardia; chronic renal disease; thyroid disorder;
KW   inflammation; asthma; hypertensive; antiarrhythmic; antiinflammatory;
KW   receptor.
XX
OS   Homo sapiens.
XX
PN   US2002137887-A1.
XX
PD   26-SEP-2002.
XX
PF   17-JAN-2001; 2001US-0765034.
XX
PR   17-JAN-2001; 2001US-0765034.
XX
PA   (HEDR/) HEDRICK J A.
PA   (LACH/) LACHOWICZ J E.
```

PA (WANG/) WANG W.
PA (GUST/) GUSTAFSON E L.
XX
PI Hedrick JA, Lachowicz JE, Wang W, Gustafson EL;
XX
DR WPI; 2003-074992/07.
DR N-PSDB; ABS57291.
XX
PT Novel isolated mammalian adenosine receptor polypeptide useful for
PT identifying an agonist or antagonist of the receptor for treating
PT vasodilation, hypotension, chronic renal diseases, thyroid disorders
PT and inflammation -
XX
PS Claim 2; Page 16-17; 19pp; English.
XX
CC The present invention relates to the isolation of a mammalian
CC (human) adenosine receptor, and the polynucleotide sequence
CC encoding it. The cloned receptor resembles a member of the
CC G-protein coupled receptor (GPCR) superfamily that contains
CC 7-transmembrane domains. The adenosine receptor is useful for
CC identifying agonists and antagonists of the receptor, which may be
CC useful for treating an adenosine-mediated medical condition. The
CC adenosine receptor polypeptide sequence is also useful as an
CC antigen to elicit antibody production in an immunologically
CC competent host. An antibody which binds specifically to the
CC adenosine receptor is useful for treating medical conditions caused
CC or mediated by adenosine such as vasodilation, hypotension, reversal
CC of tachycardia, chronic renal diseases, thyroid disorders and
CC inflammation (e.g. asthma). The antibody can also be used to purify
CC the adenosine receptor, or as a basis for immunoassays of the receptor.
CC The polynucleotide sequence encoding the adenosine receptor is useful
CC for producing vectors and host cells containing the vectors. It is
CC also useful for measuring expression of a mammalian adenosine
CC receptor gene in a biological sample. The present sequence represents
CC human adenosine receptor.
XX
SQ Sequence 334 AA;

Query Match 74.6%; Score 1231.5; DB 24; Length 334;
Best Local Similarity 71.8%; Pred. No. 1.9e-115;
Matches 227; Conservative 42; Mismatches 46; Indels 1; Gaps 1;

```
Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              || | :|:|||| || | ||||| || |||: |:||| ||:||:| :|||||||:|||
Db          5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:|||| ||||||||||||| ||||||||||||:|||::
Db         65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||| ||||||||||||:| |||||:||:| || | : |: | |:||||:| :|
Db        125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||:|||||||||| |||||||: :|||:|::| ||||||:|| ||::||||||:
Db        185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVP 244
```

```
Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:|||||| || |  |||  | | | :|||||||| |||:||||:|||:|:
Db        245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRD 304

Qy        300 MLISKFRQYFKSLTSF 315
              ||::: |  |||||||
Db        305 MLMNQLRHNFKSLTSF 320


RESULT 9
AAW19854
ID   AAW19854 standard; Protein; 334 AA.
XX
AC   AAW19854;
XX
DT   11-SEP-1997  (first entry)
XX
DE   Human purinergic receptor P2U2.
XX
KW   P2U2 receptor; purinergic receptor; diagnosis; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          1..23
FT                   /label= N-terminal_domain
FT   Domain          24..49
FT                   /label= TMI
FT                   /note= "transmembrane domain I"
FT   Domain          50..60
FT                   /label= ICDI
FT                   /note= "intracellular domain I"
FT   Domain          61..82
FT                   /label= TMII
FT                   /note= "transmembrane domain II"
FT   Domain          83..99
FT                   /label= ECDI
FT                   /note= "extracellular domain I"
FT   Domain          100..119
FT                   /label= TMIII
FT                   /note= "transmembrane domain III"
FT   Domain          120..141
FT                   /label= ICDII
FT                   /note= "intracellular domain II"
FT   Domain          142..161
FT                   /label= TMDIV
FT                   /note= "transmembrane domain IV"
FT   Domain          162..183
FT                   /label= ECDII
FT                   /note= "extracellular domain II"
FT   Domain          184..207
FT                   /label= TMDV
FT                   /note= "transmembrane domain V"
FT   Domain          208..233
FT                   /label= ICDIII
FT                   /note= "intracellular domain III"
```

```
FT   Domain          234..256
FT                   /label= TMDVI
FT                   /note= "transmembrane domain VI"
FT   Domain          257..276
FT                   /label= ECDIII
FT                   /note= "extracellular domain III"
FT   Domain          277..300
FT                   /label= TMDVII
FT                   /note= "transmembrane domain VII"
FT   Domain          301..334
FT                   /label= C-terminal_domain
XX
PN   WO9720045-A2.
XX
PD   05-JUN-1997.
XX
PF   08-NOV-1996;    96WO-US18175.
XX
PR   15-NOV-1995;    95US-0559524.
PR   15-NOV-1995;    95US-0006782.
XX
PA   (CORT-) COR THERAPEUTICS INC.
XX
PI   Conley PB,  Jantzen H;
XX
DR   WPI; 1997-310601/28.
DR   N-PSDB; AAT71900.
XX
PT   New isolated purinergic receptor sub-type  - used to develop
PT   products for diagnosis and therapy, e.g. for screening for agonists
PT   and antagonists which can modulate activation
XX
PS   Claim 1; Fig 1A-B; 36pp; English.
XX
CC   P2U2 receptor (AAW19854) is a novel human purinergic receptor
CC   subtype that is abundantly expressed in kidney and in many cell
CC   lines of megakaryocytic or erythroleukaemic origin and which is
CC   activated by ATP, UDP, UTP and UDP.  Its amino acid sequence was
CC   deduced from a cDNA clone derived from DAMI (ATCC CRL 9792) cells.
CC   P2U2 and its polypeptides can be expressed in host cells and used
CC   to develop diagnostic and therapeutic agents.  Antagonists and
CC   agonists based on the extracellular domains of P2U2 receptor, or
CC   which affect receptor function by binding to one of the
CC   intracellular domains, can be used to treat diseases caused by
CC   aberrant activation of this receptor or to treat diseases whose
CC   symptoms can be ameliorated by stimulating or inhibiting the
CC   activity of the receptor.
XX
SQ   Sequence   334 AA;

  Query Match             74.3%;  Score 1226.5;  DB 18;  Length 334;
  Best Local Similarity   71.5%;  Pred. No. 6.2e-115;
  Matches  226;  Conservative   42;  Mismatches   47;  Indels    1;  Gaps    1;

Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              || | :|:|||| || | ||||| || |||: |:|||  ||:||:| :|||||||:||||
Db          5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64
```

```
Qy          61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
               ||:|| |||||||:||:||||    |||||||||||||| |||||||||||||:||||::
Db          65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy         121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
               ||||||| ||||||||||||:| |||||:||:|  || |  : |: | |:||||:| :|
Db         125 KYPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy         181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
               ||||:|||||||||| ||||||||: :|||:|::| ||||||:||  ||::||||||:|
Db         185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVL 244

Qy         241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
               |||||:|||:|||||| || |  |||  | | | :|| | |||| |||:||||:|||:|:
Db         245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRALGFLNSVINPVFYFLLGDHFRD 304

Qy         300 MLISKFRQYFKSLTSF 315
               ||::: |  |||||||
Db         305 MLMNQLRHNFKSLTSF 320
```

```
RESULT 10
AAW22732
ID   AAW22732 standard; Protein; 334 AA.
XX
AC   AAW22732;
XX
DT   07-OCT-1997  (first entry)
XX
DE   Human ATP receptor.
XX
KW   ATP receptor; G-protein coupled receptor; agonist; antagonist.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 212
FT                   /note= "encoded by TCC"
FT   Misc-difference 235
FT                   /note= "encoded by TCG"
FT   Misc-difference 244
FT                   /label= Unknown
FT                   /note= "encoded by CYT"
XX
PN   WO9724929-A1.
XX
PD   17-JUL-1997.
XX
PF   11-JAN-1996;   96WO-US00392.
XX
PR   11-JAN-1996;   96WO-US00392.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Li Y;
XX
```

DR WPI; 1997-372505/34.
DR N-PSDB; AAT75146.
XX
PT Isolated human ATP receptor - agonists and antagonists of which are
PT useful in treatment of, e.g. asthma, hypertension, arterial
PT thrombosis and psychotic and neurological disorders
XX
PS Claim 15; Fig 1A-C; 53pp; English.
XX
CC Human ATP receptor (AAW22732) is structurally related to the G
CC protein-coupled receptor family. It shows 29.8% identity to a
CC murine P2u receptor. Its amino acid sequence was deduced from a
CC human placental cDNA clone (AAT75146). Recombinant ATP receptor can
CC be expressed in bacterial (e.g. E. coli), mammalian (e.g. COS) or
CC insect (e.g. Sf9) host cells and used to screen for agonists and
CC antagonists useful in the treatment of conditions related to
CC underexpression of the receptor (e.g. asthma, Parkinson's disease,
CC acute heart failure, hypotension, urinary retention and
CC osteoporosis) or underexpression of the receptor (e.g. arterial
CC thrombosis, hypertension, thrombolysis, angioplasty, cystic
CC fibrosis, ulcers, asthma, allergy, benign prostatic hypertrophy,
CC psychotic and neurological disorders, dyskinesias, endogenous
CC anorexia and bulimia).
XX
SQ Sequence 334 AA;

Query Match 73.9%; Score 1219.5; DB 18; Length 334;
Best Local Similarity 71.2%; Pred. No. 3.1e-114;
Matches 225; Conservative 43; Mismatches 47; Indels 1; Gaps 1;

```
Qy          1 MAQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              || | :|:|||| || | ||||| || |||: |:||| ||:||:| :|||||||:||||
Db          5 MAWNATCKNWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFN 64

Qy         61 LSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLM 120
              ||:|| |||||||:||:|||| ||||||||||||| ||||||||||||:||||::
Db         65 LSVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLII 124

Qy        121 KYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHN 180
              ||||||| ||||| |||||||:| |||||:||:|  || |  : |: | |:||||:| :|
Db        125 KYPFREHLLQKKECAILISLAMWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYN 184

Qy        181 LIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSIL 240
              ||||:|||||||||| |||||||: :|||:|::| ||||||:||  ||::||||||:
Db        185 LIYSMCLTLLGFLIPLFVMCFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVX 244

Qy        241 FTPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE 299
              |||||:|||:|||||| || |  |||  | | | :|||:|||||  |||:||||:|||:|:
Db        245 FTPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPVAFLNSVINPVFYFLVGDHFRD 304

Qy        300 MLISKFRQYFKSLTSF 315
              ||::: |  |||||||
Db        305 MLMNQLRHNFKSLTSF 320
```

RESULT 11
AAU31029

ID AAU31029 standard; Protein; 387 AA.
XX
AC AAU31029;
XX
DT 18-DEC-2001 (first entry)
XX
DE Novel human secreted protein #1520.
XX
KW Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
PN WO200179449-A2.
XX
PD 25-OCT-2001.
XX
PF 16-APR-2001; 2001WO-US08656.
XX
PR 18-APR-2000; 2000US-0552929.
PR 26-JAN-2001; 2001US-0770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy -
XX
PS Claim 20; Page 392; 765pp; English.
XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX
SQ Sequence 387 AA;

Query Match 73.7%; Score 1216.5; DB 22; Length 387;
Best Local Similarity 71.1%; Pred. No. 7.6e-114;
Matches 224; Conservative 43; Mismatches 47; Indels 1; Gaps 1;

```
Qy          2 AQNLSCENWLATEAILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNL 61
              | | :|::||| || | ||||| || |||: |:|||  ||:||:| :||||||||:|||||
Db         59 AWNATCKHWLAAEAALEKYYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFNL 118

Qy         62 SISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMK 121
              |:|| |||||||:||:||||    |||||||||||||| ||||||||||||:||||::|
Db        119 SVSDLAFLCTLPMLIRSYANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLIIK 178

Qy        122 YPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNL 181
              |||||| |||||||||||||:| |||||:||:|  || |  : |: | |:||||:| :||
Db        179 YPFREHLLQKKEFAILISLAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYNL 238

Qy        182 IYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSILF 241
              |||:|||||| ||| ||| |||||: :|||:|::| ||||||:||  ||::||||||:||
Db        239 IYSMCLTLLGFSIPLFVMCLFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVLF 298

Qy        242 TPYHIMRNLRIASRLDSWPQ-GCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREM 300
              ||||:|||:|||||| || |  |||  | | | :|||||||| |||:||||:|||:|:|
Db        299 TPYHVMRNVRIASRLGSWKQYQCTQVVINSFYIVTRPLAFLNSVINPVFYFLLGDHFRDM 358

Qy        301 LISKFRQYFKSLTSF 315
              |::: |  |||||||
Db        359 LMNQLRHNFKSLTSF 373
```

RESULT 12
AAB45376
ID AAB45376 standard; Protein; 258 AA.
XX
AC AAB45376;
XX
DT 14-FEB-2001 (first entry)
XX
DE Human secreted protein sequence encoded by gene 37 SEQ ID NO:128.
XX
KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; vulnerary; gene therapy; autoimmune disease;
KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;
KW cerebrovascular disorder; nervous system disorder; infection; skin aging;
KW ocular disorder; wound healing; food additive; preservative.
XX
OS Homo sapiens.
XX
PN WO200061628-A1.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US09070.
XX
PR 09-APR-1999; 99US-0128695.
PR 14-JAN-2000; 2000US-0176052.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX

PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-619228/59.
XX
PT New nucleic acid molecules encoding 49 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives -
XX
PS Disclosure; Page 447-448; 454pp; English.
XX
CC The polynucleotide sequences given in AAC81086 to AAC81134 encode the
CC human secreted proteins given in AAB45308 to AAB45356. AAB45357 to
CC AAB45384 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Examples of activities include:
CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative;
CC cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
CC neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
CC and vulnerary. The polynucleotides and polypeptides can be used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Disorders which are diagnosed or treated include
CC autoimmune diseases, hyperproliferative disorders, cardiovascular
CC disorders, cerebrovascular disorders, angiogenesis, nervous system
CC disorders, infections caused by bacteria, viruses and fungi and ocular
CC disorders. The polypeptides can also be used to aid wound healing and
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to
CC maintain organs before transplantation, for supporting cell culture of
CC primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors and other nutritional
CC components. AAC81077 to AAC81085 and AAB45307 represent sequences used in
CC the exemplification of the present invention.
XX
SQ Sequence 258 AA;

Query Match 61.5%; Score 1014.5; DB 21; Length 258;
Best Local Similarity 72.9%; Pred. No. 9.7e-94;
Matches 188; Conservative 33; Mismatches 36; Indels 1; Gaps 1;

```
Qy         20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
              |||| || |||: |:|||  ||:||:| :|||||||:||||||:|| |||||||:||:||
Db          1 YYLSIFYGIEFVVGVLGNTIVVYGYIFSLKNWNSSNIYLFNLSVSDLAFLCTLPMLIRSY 60

Qy         80 ANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILIS 139
              ||    |||||||||||||| ||||||||||||:||||::||||||| ||||||||||
Db         61 ANGNWIYGDVLCISNRYVLHANLYTSILFLTFISIDRYLIIKYPFREHLLQKKEFAILIS 120

Qy        140 LAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
              ||:| |||||:||:|  || |  : |: | |:||||:| :|||||:||||||||||| ||
Db        121 LAIWVLVTLELLPILPLINPVITDNGTTCNDFASSGDPNYNLIYSMCLTLLGFLIPLFVM 180

Qy        200 CFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIASRLDSW 259
              ||||||: :|||:|::| ||||||:||  ||::|||||:||||||:|||:|||||| ||
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```
Db        181 CFFYYKIALFLKQRNRQVATALPLEKPLNLVIMAVVIFSVLFTPYHVMRNVRIASRLGSW 240

Qy        260 PQ-GCTQKAIKSIYTLTR 276
                |  |||  | | | :||
Db        241 KQYQCTQVVINSFYIVTR 258


RESULT 13
ABP54317
ID   ABP54317 standard; Protein; 373 AA.
XX
AC   ABP54317;
XX
DT   16-JAN-2003  (first entry)
XX
DE   Rat P2Y purinoceptor 1 protein SEQ ID NO:7.
XX
KW   Human; G protein coupled receptor; GPCR; HGPRBMY27; antiinflammatory;
KW   antiinfertility; pulmonary; cytostatic; nephrotropic; hormonal;
KW   circulatory; gene therapy; inflammatory disorder; reproductive disorder;
KW   pulmonary disorder; cancer; renal disorder; connective tissue disorder;
KW   endocrine disorder.
XX
OS   Rattus norvegicus.
XX
PN   WO200272755-A2.
XX
PD   19-SEP-2002.
XX
PF   06-MAR-2002; 2002WO-US06796.
XX
PR   07-MAR-2001; 2001US-273808P.
PR   07-MAR-2001; 2001US-278983P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Ramanathan C,  Feder J,  Mintier G,  Cacace A,  Barber L;
XX
DR   WPI; 2002-657945/70.
XX
PT   New polynucleotide encoding a human G-protein coupled receptor for
PT   preventing, treating, or ameliorating e.g. an inflammatory,
PT   reproductive, pulmonary, renal connective tissue, or endocrine disorder
PT
XX
PS   Disclosure; Fig 2A-B; 356pp; English.
XX
CC   The present invention describes a human G protein coupled receptor
CC   (GPCR), designated HGPRBMY27 (I). (I) has antiinflammatory,
CC   antiinfertility, pulmonary, cytostatic, nephrotropic, hormonal and
CC   circulatory activities, and can be used in gene therapy. (I) or the
CC   protein encoded by it can be used to prevent, treat, or ameliorate a
CC   medical condition, such as inflammatory disorders, reproductive
CC   disorders, pulmonary disorders, cancer, renal disorders, connective
CC   tissue disorders, endocrine disorders, or disorders involving
CC   aberrations in tubular tissues. They can also be used to diagnose a
CC   pathological condition or a susceptibility to (I). The protein can
```

CC be used to screen for candidate compounds capable of modulating activity
CC of a GPCR polypeptide. The present sequence represents a GPCR given in
CC comparison with the HGPRBMY27 protein in the exemplification of the
CC present invention.
XX
SQ Sequence 373 AA;

Query Match 29.0%; Score 479; DB 23; Length 373;
Best Local Similarity 37.3%; Pred. No. 1.3e-39;
Matches 107; Conservative 57; Mismatches 115; Indels 8; Gaps 6;

```
Qy         20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
              ||| | | : || | |||   :: ::| || |:  :||:|||:::|| :: ||| ||  |
Db         52 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 111

Qy         80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
               |     :|||:|   |:: | ||| |||||| ||  ||  : || :     ||: || :
Db        112 FNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAIYV 171

Qy        139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
              |: || :| : : |:| :  : : | :   | |  |        |||:| |:  | |||
Db        172 SVLVWLIVVVAISPILFYSGTGIRKNKTVTCYDSTSDEYLRSYFIYSMCTTVAMFCIPLV 231

Qy        198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
              ::   | :|  | :    :   ||  |   ||:: : :|:: : |:|:|: : : :||
Db        232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 288

Qy        257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
              |  |: |    : : | :|| || ||| ::|| ||| || :|  |
Db        289 DFQTPEMCDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335
```

RESULT 14
ABU11903
ID ABU11903 standard; Protein; 373 AA.
XX
AC ABU11903;
XX
DT 13-FEB-2003 (first entry)
XX
DE Rat purinergic receptor.
XX
KW Receptor; HGPREMY11; HGPRBMY11v1; HGPRBMY11v2; GPCR74; GPCR81;
KW G-protein coupled receptor; cardiovascular disease; arrhythmia;
KW myocardial infarction; congestive heart failure; cardiomyopathy;
KW atherosclerosis; arteriosclerosis; embolism; angina; thrombosis;
KW hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis;
KW obesity; human immunodeficiency virus infection; HIV; schizophrenia;
KW sleeplessness; acquired immunodeficiency syndrome; AIDS; leukaemia;
KW sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia.
XX
OS Rattus norvegicus.
XX
PN WO200286123-A2.
XX
PD 31-OCT-2002.
XX

PF 16-NOV-2001; 2001WO-US44019.
XX
PR 17-NOV-2000; 2000US-249613P.
PR 21-DEC-2000; 2000US-257611P.
PR 16-JUL-2001; 2001US-305818P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Feder J, Nelson TC, Ramanathan C, Cacace AM, Barber LE;
XX
DR WPI; 2003-093137/08.
XX
PT New human G-protein coupled receptor HGPRBMY11 polypeptide or
PT polynucleotide, useful for preventing, treating or ameliorating e.g.
PT myocardial infarction, angina, thrombosis, Alzheimer's disease,
PT schizophrenia, AIDS, leukemia -
XX
PS Disclosure; Fig 2; 444pp; English.
XX
CC The invention relates to an isolated polypeptide (designated HGPRBMY11),
CC which has a G-protein coupled receptor (GPCR) activity (also known
CC as GPCR74 or GPCR81) and is encoded by the cDNA contained in ATCC Deposit
CC Number PTA-2766, its variants (HGPRBMY11v1 and HGPRBMY11v2), fragments,
CC domains, species homologues and proteins 95% similar to it. Also included
CC are: (1) the nucleic acids encoding the HGPRBMY11 proteins (including
CC variants, fragments, complements and sequences 95% similar to the
CC HGPRBMY11 nucleic acids); (2) recombinant vectors; (3) transformed host
CC cells expressing HGPRBMY11; (4) an anti-HGPRBMY11 antibody; (5)
CC diagnosing a pathological condition or a susceptibility to a pathological
CC condition in a subject; (6) identifying a binding partner to the
CC HGPRBMY11 polypeptide; (7) identifying an activity in a biological assay;
CC (8) a process for making polynucleotide sequences encoding a gene product
CC having altered GPCR activity; (9) a shuffled polynucleotide produced by
CC the method of (8); and (10) screening for candidate compounds capable of
CC binding to and/or modulating activity of a GPCR. The polypeptide or the
CC polynucleotide is useful for preventing, treating or ameliorating a
CC medical condition, particularly cardiovascular diseases or disorders,
CC e.g. myocardial infarction, congestive heart failure, arrhythmias,
CC cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina,
CC thrombosis or hypertension). The HGPRBMY11 polypeptide or polynucleotide
CC is also useful for treating, preventing or ameliorating e.g. Alzheimer's
CC disease, Parkinson's disease, osteoporosis, obesity, human
CC immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness,
CC acquired immunodeficiency syndrome (AIDS), leukaemia, sepsis,
CC inflammations, psoriasis, Gaucher's disease or ischaemia (many
CC other diseases and disorders are listed in the specification).
CC The present sequence represents a homologue of an HGPRBMY11 protein
CC (or variant).
XX
SQ Sequence 373 AA;

Query Match 29.0%; Score 479; DB 24; Length 373;
Best Local Similarity 37.3%; Pred. No. 1.3e-39;
Matches 107; Conservative 57; Mismatches 115; Indels 8; Gaps 6;

Qy 20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79

```
Db         52 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 111

Qy         80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
                |     :|||:|   |:: | ||| |||||| ||  ||  : || :     ||: || :
Db        112 FNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAIYV 171

Qy        139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
              |: || :| : : |:| :  : : | :   | |  |        |||:| |:  | |||
Db        172 SVLVWLIVVVAISPILFYSGTGIRKNKTVTCYDSTSDEYLRSYFIYSMCTTVAMFCIPLV 231

Qy        198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
              ::   |  :|  |  :    :   ||  |   ||:: : :|:: : |:|:|: : : :||
Db        232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 288

Qy        257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
              |   |: |     : : | :|| || ||| ::|| ||| || :|  |
Db        289 DFQTPEMCDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335
```

```
RESULT 15
AAE04389
ID   AAE04389 standard; Protein; 373 AA.
XX
AC   AAE04389;
XX
DT   04-SEP-2001  (first entry)
XX
DE   Human P2-purinergic receptor subtype, P2Y1.
XX
KW   Human; P2-purinergic receptor; P2Y1; cardiant; vasotropic; thrombolytic;
KW   cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina;
KW   myocardial infarction; ischaemic attack; preeclampsia; bleeding disorder;
KW   carotid endarterectomy; vascular graft surgery; brain disorder; migraine;
KW   vascular injury; schizophrenia; eating disorder; depression; angioplasty;
KW   peripheral vascular disease; platelet aggregation; restenotic; embolism;
KW   thrombocytopaenic purpura; stroke; pertussis toxin-sensitive G protein;
KW   Gi; disseminated intravascular coagulation; thrombosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          53..76
FT                   /label= Transmembrane_domain_1
FT   Domain          84..109
FT                   /label= Transmembrane_domain_2
FT   Domain          124..148
FT                   /label= Transmembrane_domain_3
FT   Domain          167..190
FT                   /label= Transmembrane_domain_4
FT   Domain          217..241
FT                   /label= Transmembrane_domain_5
FT   Domain          258..283
FT                   /label= Transmembrane_domain_6
FT   Domain          304..329
FT                   /label= Transmembrane_domain_7
XX
PN   WO200146454-A1.
```

XX
PD 28-JUN-2001.
XX
PF 26-DEC-2000; 2000WO-US34998.
XX
PR 23-DEC-1999; 99US-0171622.
XX
PA (CORT-) COR THERAPEUTICS INC.
XX
PI Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;
PI Hollopeter G;
XX
DR WPI; 2001-418082/44.
XX
PT Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful
PT for identifying binding partners and for diagnostic applications -
XX
PS Disclosure; Fig 5A; 108pp; English.
XX
CC The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed
CC as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is
CC the subtype of P2-purinergic receptor. The P2Y12 receptor is expressed
CC selectively in the platelets and brain, and couples to a pertussis toxin-
CC sensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor
CC that responds to ADP. The invention also relates to a method for
CC identifying an agent which is useful for modulating acute myocardial
CC infarction, unstable angina, chronic stable angina, transient ischaemic
CC attacks, strokes, peripheral vascular disease, preeclampsia, deep venous
CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic
CC thrombocytopaenic purpura or a bleeding disorder; thrombotic and
CC restenotic complications following angioplasty, carotid endarterectomy,
CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery,
CC stent placements or insertion of endovascular devices and prostheses.
CC P2Y12 receptor is useful for identifying binding partners and for
CC diagnostic applications. P2Y12 receptor provides targets for screening
CC synthetic small molecules and combinatorial or naturally occurring
CC compound libraries to regulate platelet aggregation, vascular injury, or
CC disease as well as schizophrenia, eating disorders, depression, migraine
CC and other brain disorders. The present sequence is human P2-purinergic
CC receptor subtype, P2Y1 related to the invention.
XX
SQ Sequence 373 AA;

Query Match 28.7%; Score 474; DB 22; Length 373;
Best Local Similarity 37.3%; Pred. No. 4.2e-39;
Matches 107; Conservative 55; Mismatches 117; Indels 8; Gaps 6;

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Qy          20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
               ||| | | : || | |||   :: ::| || |:  :||:|||:::|| :: ||| ||  |
Db          52 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 111

Qy          80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
                |     :|| :|   |:: | ||| |||||| ||  ||  : || :     ||: || |
Db         112 FNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAICI 171

Qy         139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
               |: || :| : : |:| :  : | | :   | |  |        |||:| |:  | :||
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```
Db        172 SVLVWLIVVVAISPILFYSGTGVRKNKTITCYDTTSDEYLRSYFIYSMCTTVAMFCVPLV 231

Qy        198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
              ::   |  :|  |  :    :   ||  |   ||:: : :|:: : |:|:|: : : :||
Db        232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 288

Qy        257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
              |   |  |     : : | :|| || ||| ::|| ||| || :|  |
Db        289 DFQTPAMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335
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Search completed: December 12, 2003, 18:07:09
Job time : 42 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 12, 2003, 17:58:52 ; Search time 18 Seconds
(without alignments)
828.193 Million cell updates/sec

Title: US-09-891-138A-2
Perfect score: 1650
Sequence: 1 MAQNLSCENWLATEAILNKY.....REMLISKFRQYFKSLTSFRT 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	479	29.0	373	1	P2YR_RAT	P49651 rattus norv
2	475	28.8	373	1	P2YR_MOUSE	P49650 mus musculu
3	474	28.7	373	1	P2YR_BOVIN	P48042 bos taurus
4	474	28.7	373	1	P2YR_HUMAN	P47900 homo sapien
5	472.5	28.6	362	1	P2YR_CHICK	P34996 gallus gall
6	472.5	28.6	362	1	P2YR_MELGA	P49652 meleagris g
7	386.5	23.4	537	1	P2Y8_XENLA	P79928 xenopus lae
8	379.5	23.0	328	1	P2Y3_CHICK	Q98907 gallus gall
9	374	22.7	374	1	P2Y2_RAT	P41232 rattus norv
10	373.5	22.6	373	1	P2Y2_MOUSE	P35383 mus musculu
11	371.5	22.5	328	1	P2Y3_MELGA	O93361 meleagris g
12	363.5	22.0	377	1	P2Y2_HUMAN	P41231 homo sapien
13	354	21.5	361	1	P2Y4_RAT	O35811 rattus norv
14	353	21.4	355	1	C3X1_HUMAN	P49238 homo sapien
15	352	21.3	365	1	P2Y4_HUMAN	P51582 homo sapien
16	343	20.8	361	1	P2Y4_MOUSE	Q9jjs7 mus musculu
17	336.5	20.4	360	1	CKR4_HUMAN	P51679 homo sapien

18	336	20.4	328	1	P2Y6_RAT	Q63371 rattus norv
19	333	20.2	308	1	P2Y5_CHICK	P32250 gallus gall
20	332.5	20.2	354	1	C3X1_RAT	P35411 rattus norv
21	332	20.1	328	1	P2Y6_HUMAN	Q15077 homo sapien
22	329	19.9	355	1	CKR1_MACMU	P56482 macaca mula
23	328	19.9	355	1	CKR1_HUMAN	P32246 homo sapien
24	326.5	19.8	346	1	CLT2_HUMAN	Q9ns75 homo sapien
25	326.5	19.8	360	1	CKR4_MOUSE	P51680 mus musculu
26	325.5	19.7	354	1	C3X1_MOUSE	Q9z0d9 mus musculu
27	325.5	19.7	388	1	SSR4_HUMAN	P31391 homo sapien
28	319.5	19.4	345	1	CLT2_PIG	Q95n03 sus scrofa
29	319	19.3	353	1	APJ_XENLA	P79960 xenopus lae
30	318.5	19.3	359	1	IL8B_MOUSE	P35343 mus musculu
31	317.5	19.2	355	1	GPR1_HUMAN	P46091 homo sapien
32	317	19.2	368	1	SSR2_BOVIN	P34993 bos taurus
33	316.5	19.2	384	1	SSR4_RAT	P30937 rattus norv
34	315.5	19.1	355	1	GPR1_MACMU	O97664 macaca mula
35	315.5	19.1	355	1	IL8A_RABIT	P21109 oryctolagus
36	315	19.1	355	1	CKR8_HUMAN	P51685 homo sapien
37	314	19.0	369	1	SSR2_HUMAN	P30874 homo sapien
38	314	19.0	369	1	SSR2_PIG	P34994 sus scrofa
39	314	19.0	370	1	P2Y9_HUMAN	Q99677 homo sapien
40	313.5	19.0	353	1	IL8B_PANTR	Q28807 pan troglod
41	313.5	19.0	356	1	CKR8_MACMU	O97665 macaca mula
42	313.5	19.0	356	1	IL8B_CANFA	O97571 canis famil
43	313	19.0	344	1	P2Y5_HUMAN	P43657 homo sapien
44	312.5	18.9	360	1	IL8B_HUMAN	P25025 homo sapien
45	311.5	18.9	309	1	CLT2_MOUSE	Q920a1 mus musculu

ALIGNMENTS

```
RESULT 1
P2YR_RAT
ID   P2YR_RAT       STANDARD;      PRT;   373 AA.
AC   P49651;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   01-FEB-1996 (Rel. 33, Last annotation update)
DE   P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN   P2RY1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Insulinoma;
RX   MEDLINE=95298025; PubMed=7779087;
RA   Tokuyama Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;
RT   "Cloning of rat and mouse P2Y purinoceptors.";
RL   Biochem. Biophys. Res. Commun. 211:211-218(1995).
CC   -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC       ATP AND ADP. IN PANCREATIC ISLETS, MAY MEDIATE SOME OF THE EFFECTS
CC       OF EXTRACELLULAR ATP ON INSULIN SECRETION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
```

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CC   -!- TISSUE SPECIFICITY: EXPRESSED IN MUSCLE, HEART, LIVER, KIDNEY,
CC       LUNG, BRAIN, SPLEEN, BUT NOT IN TESTIS.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U22830; AAA91303.1; -.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     52       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     53     74       1 (POTENTIAL).
FT   DOMAIN       75     87       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     88    109       2 (POTENTIAL).
FT   DOMAIN      110    126       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    127    147       3 (POTENTIAL).
FT   DOMAIN      148    166       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    167    188       4 (POTENTIAL).
FT   DOMAIN      189    218       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    219    238       5 (POTENTIAL).
FT   DOMAIN      239    265       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    266    285       6 (POTENTIAL).
FT   DOMAIN      286    303       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    304    328       7 (POTENTIAL).
FT   DOMAIN      329    373       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    124    202       BY SIMILARITY.
FT   CARBOHYD     11     11       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     27     27       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    113    113       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    197    197       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   373 AA;  42321 MW;  6DDF676287B5E648 CRC64;

  Query Match             29.0%;  Score 479;  DB 1;  Length 373;
  Best Local Similarity   37.3%;  Pred. No. 1.6e-25;
  Matches  107;  Conservative   57;  Mismatches  115;  Indels    8;  Gaps    6;

Qy         20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
              ||| | | : || | |||   :: ::| || |:  :||:|||:::|| :: ||| ||  |
Db         52 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 111

Qy         80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
               |     :|||:|   |:: | ||| |||||| ||  ||  : || :     ||: || :
Db        112 FNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAIYV 171

Qy        139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
              |: || :| : : |:| :  : : | :   | |  |        |||:| |:  | |||
Db        172 SVLVWLIVVVAISPILFYSGTGIRKNKTVTCYDSTSDEYLRSYFIYSMCTTVAMFCIPLV 231
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Qy        198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
              ::   |  :|  |  :   :   ||  |   ||:: : :|:: : |:|:|: : : :||
Db        232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 288

Qy        257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
              |   |: |     : : | :|| || ||| ::|| ||| || :|  |
Db        289 DFQTPEMCDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335


RESULT 2
P2YR_MOUSE
ID   P2YR_MOUSE     STANDARD;      PRT;   373 AA.
AC   P49650;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN   P2RY1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Insulinoma;
RX   MEDLINE=95298025; PubMed=7779087;
RA   Tokuyama Y., Hara M., Jones E.M.C., Fan Z., Bell G.I.;
RT   "Cloning of rat and mouse P2Y purinoceptors.";
RL   Biochem. Biophys. Res. Commun. 211:211-218(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/Sv;
RA   Leon C.;
RT   "Thromboresistance in P2Y1 receptor knockout mice.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC       ATP AND ADP. IN PANCREATIC ISLETS, MAY MEDIATE SOME OF THE EFFECTS
CC       OF EXTRACELLULAR ATP ON INSULIN SECRETION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U22829; AAA91302.1; -.
DR   EMBL; AJ245636; CAB57317.1; -.
DR   HSSP; P34996; 1DDD.
DR   MGD; MGI:105049; P2ry1.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
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DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     52       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     53     74       1 (POTENTIAL).
FT   DOMAIN       75     87       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     88    109       2 (POTENTIAL).
FT   DOMAIN      110    126       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    127    147       3 (POTENTIAL).
FT   DOMAIN      148    166       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    167    188       4 (POTENTIAL).
FT   DOMAIN      189    218       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    219    238       5 (POTENTIAL).
FT   DOMAIN      239    265       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    266    285       6 (POTENTIAL).
FT   DOMAIN      286    303       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    304    328       7 (POTENTIAL).
FT   DOMAIN      329    373       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    124    202       BY SIMILARITY.
FT   CARBOHYD     11     11       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     27     27       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    113    113       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    197    197       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   373 AA;  42212 MW;  944125E9F4560BB3 CRC64;

  Query Match             28.8%;  Score 475;  DB 1;  Length 373;
  Best Local Similarity   37.3%;  Pred. No. 3e-25;
  Matches  107;  Conservative   55;  Mismatches  117;  Indels    8;  Gaps    7;

Qy         20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
              ||| | | : || | |||   :: ::| || |:  :||:|||:::|| :: ||| ||  |
Db         52 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 111

Qy         80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
               |     :|| :|   |:: | ||| |||||| ||  ||  : || :     ||: || :
Db        112 FNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAIYV 171

Qy        139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
              |: || :| : : |:| :  :   | :   | |  |:       |||:| |:  | |||
Db        172 SVLVWLIVVVAISPILFYSGTGTRKNKTVTCYDTTSNDYLRSYFIYSMCTTVAMFCIPL- 230

Qy        198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
              |:    | ::|  |           ||  |   ||:: : :|:: : |:|:|: : : :||
Db        231 VLILGCYGLIV--KALIYNDLDNSPLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 288

Qy        257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
              |   |: |     : : | :|| || ||| ::|| ||| || :|  |
Db        289 DFQTPEMCDFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335


RESULT 3
P2YR_BOVIN
ID   P2YR_BOVIN     STANDARD;      PRT;   373 AA.
AC   P48042;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
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```
DE   P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN   P2RY1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Aortic endothelium;
RX   MEDLINE=95352058; PubMed=7626079;
RA   Henderson D.J., Elliot D.G., Smith G.M., Webb T.E., Dainty I.A.;
RT   "Cloning and characterisation of a bovine P2Y receptor.";
RL   Biochem. Biophys. Res. Commun. 212:648-656(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Corpus callosum;
RX   MEDLINE=99064562; PubMed=9848096;
RA   Deng G., Matute C., Kumar C.K., Fogarty D.J., Miledi R.;
RT   "Cloning and expression of a P2y purinoceptor from the adult bovine
RT   corpus callosum.";
RL   Neurobiol. Dis. 5:259-270(1998).
CC   -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC       ATP AND ADP.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X87628; CAA60958.1; -.
DR   EMBL; U34041; AAC78275.1; -.
DR   PIR; JC4162; JC4162.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     52       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     53     74       1 (POTENTIAL).
FT   DOMAIN       75     87       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     88    109       2 (POTENTIAL).
FT   DOMAIN      110    126       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    127    147       3 (POTENTIAL).
FT   DOMAIN      148    166       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    167    188       4 (POTENTIAL).
FT   DOMAIN      189    218       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    219    238       5 (POTENTIAL).
FT   DOMAIN      239    265       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    266    285       6 (POTENTIAL).
```

```
FT   DOMAIN       286    303       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     304    328       7 (POTENTIAL).
FT   DOMAIN       329    373       CYTOPLASMIC (POTENTIAL).
FT   DISULFID     124    202       BY SIMILARITY.
FT   CARBOHYD      11     11       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      27     27       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     113    113       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     197    197       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   373 AA;  42287 MW;  9270A7175C0BDA76 CRC64;

  Query Match             28.7%;  Score 474;  DB 1;  Length 373;
  Best Local Similarity   36.6%;  Pred. No. 3.5e-25;
  Matches  105;  Conservative   58;  Mismatches  116;  Indels    8;  Gaps    6;

Qy         20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
              ||| | | : || | |||   :: ::| || |:  :||:|||:::|| :: ||| ||  |
Db         52 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 111

Qy         80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
               |     :|| :|   |:: | ||| |||||| ||  ||  : || :     ||: |: |
Db        112 FNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAVYI 171

Qy        139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
              |: || :| : : |:| :  : : | :   | |  |        |||:| |:  | :||
Db        172 SVLVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSMCTTVAMFCVPLV 231

Qy        198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
              ::   | :|  | :    :   ||  |   ||:: : :|:: : |:|:|: : : :||
Db        232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 288

Qy        257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
              |   |: |     : : | :|| || ||| ::|| ||| || :|  |
Db        289 DFQTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335


RESULT 4
P2YR_HUMAN
ID   P2YR_HUMAN     STANDARD;      PRT;   373 AA.
AC   P47900;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN   P2RY1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=96257237; PubMed=8666290;
RA   Leon C., Vial C., Cazenave J.-P., Gachet C.;
RT   "Cloning and sequencing of a human cDNA encoding endothelial P2Y1
RT   purinoceptor.";
RL   Gene 171:295-297(1996).
RN   [2]
```

```
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96158962; PubMed=8579591;
RA   Ayyanathan K., Tania W., Harbansjit S., Raghbir A.S., Barnard E.A.,
RA   Kunapuli S.P.;
RT   "Cloning and chromosomal localization of the human P2Y1
RT   purinoceptor.";
RL   Biochem. Biophys. Res. Commun. 218:783-788(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96205320; PubMed=8630005;
RA   Janssens R., Communi D., Pirotton S., Samson M., Parmentier M.,
RA   Boeynaems J.M.;
RT   "Cloning and tissue distribution of the human P2Y1 receptor.";
RL   Biochem. Biophys. Res. Commun. 221:588-593(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Leon C., Vial C., Weber J., Cazenave J.-P., Gacher C.;
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 95-373 FROM N.A., FUNCTION, AND INHIBITION STUDIES.
RC   TISSUE=Platelet;
RX   MEDLINE=98113162; PubMed=9442040;
RA   Jin J., Daniel J.L., Kunapuli S.P.;
RT   "Molecular basis for ADP-induced platelet activation. II. The P2Y1
RT   receptor mediates ADP-induced intracellular calcium mobilization and
RT   shape change in platelets.";
RL   J. Biol. Chem. 273:2030-2034(1998).
CC   -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC       ATP AND ADP. IN PLATELETS BINDING TO ADP LEADS TO MOBILIZATION OF
CC       INTRACELLULAR CALCIUM IONS VIA ACTIVATION OF PHOSPHOLIPASE C, A
CC       CHANGE IN PLATELET SHAPE, AND PROBABLY TO PLATELET AGGREGATION.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- INDUCTION: REPRESSED BY THE P2Y1 RECEPTOR-SPECIFIC ANTAGONISTS
CC       A3P5PS, A3P5P AND A2P5P. THESE INHIBIT CALCIUM ION MOBILIZATION
CC       AND SHAPE CHANGE IN PLATELETS.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Z49205; CAA89066.1; -.
DR   EMBL; U42030; AAA97873.1; -.
DR   EMBL; U42029; AAA97872.1; -.
DR   EMBL; S81950; AAB47091.1; -.
DR   EMBL; AJ006945; CAA07339.1; -.
DR   EMBL; AF018284; AAB94556.1; -.
DR   PIR; JC4737; JC4737.
DR   HSSP; P34996; 1DDD.
DR   Genew; HGNC:8539; P2RY1.
DR   MIM; 601167; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
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DR   GO; GO:0004872; F:receptor activity; TAS.
DR   GO; GO:0007200; P:G-protein signaling, coupled to IP3 second . . .; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; Platelet;
KW   Blood coagulation.
FT   DOMAIN        1     52       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     53     74       1 (POTENTIAL).
FT   DOMAIN       75     87       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     88    109       2 (POTENTIAL).
FT   DOMAIN      110    126       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    127    147       3 (POTENTIAL).
FT   DOMAIN      148    166       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    167    188       4 (POTENTIAL).
FT   DOMAIN      189    218       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    219    238       5 (POTENTIAL).
FT   DOMAIN      239    265       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    266    285       6 (POTENTIAL).
FT   DOMAIN      286    303       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    304    328       7 (POTENTIAL).
FT   DOMAIN      329    373       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    124    202       BY SIMILARITY.
FT   CARBOHYD     11     11       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     27     27       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    113    113       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    197    197       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    138    138       MISSING (IN REF. 1).
SQ   SEQUENCE   373 AA;  42071 MW;  4DC7C668B4145392 CRC64;

  Query Match             28.7%;  Score 474;  DB 1;  Length 373;
  Best Local Similarity   37.3%;  Pred. No. 3.5e-25;
  Matches  107;  Conservative   55;  Mismatches  117;  Indels    8;  Gaps    6;

Qy         20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
              ||| | | : || | |||   :: ::| || |:  :||:|||:::|| :: ||| ||  |
Db         52 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 111

Qy         80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
               |     :|| :|   |:: | ||| |||||| ||  ||  : || :     ||: || |
Db        112 FNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAICI 171

Qy        139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
              |: || :| : : |:| :  : | | :   | |  |        |||:| |:  | :||
Db        172 SVLVWLIVVVAISPILFYSGTGVRKNKTITCYDTTSDEYLRSYFIYSMCTTVAMFCVPLV 231

Qy        198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
              ::   | :|  | :    :   ||  |   ||:: : :|:: : |:|:|: : : :||
Db        232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 288

Qy        257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
              |  |  |     : : | :|| || ||| ::|| ||| || :|  |
Db        289 DFQTPAMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335
```

```
RESULT 5
P2YR_CHICK
ID   P2YR_CHICK     STANDARD;      PRT;   362 AA.
AC   P34996;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor).
GN   P2RY1.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=93285340; PubMed=8508924;
RA   Webb T.E., Simon J., Krishek B.J., Bateson A.N., Smart T.G.,
RA   King B.F., Burnstock G., Barnard E.A.;
RT   "Cloning and functional expression of a brain G-protein-coupled ATP
RT   receptor.";
RL   FEBS Lett. 324:219-225(1993).
RN   [2]
RP   3D-STRUCTURE MODELING.
RX   MEDLINE=97026278; PubMed=8872457;
RA   van Rhee A.M., Fischer B., van Galen P.J.M., Jacobson K.A.;
RT   "Modelling the P2Y purinoceptor using rhodopsin as template.";
RL   Drug Des. Discov. 13:133-140(1995).
CC   -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC       ATP AND ADP. SEEMS TO MEDIATE ITS ACTION VIA A PERTUSSIS TOXIN
CC       INSENSITIVE G-PROTEIN, PROBABLY BELONGING TO THE GQ FAMILY THAT
CC       ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: BRAIN, SPINAL CORD, GASTROINTESTINAL TRACT,
CC       SPLEEN AND LEG MUSCLE. IS NOT DETECTED IN THE HEART, LIVER,
CC       STOMACH, LUNG AND KIDNEY.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X73268; CAA51716.1; -.
DR   PIR; S33733; S33733.
DR   PDB; 1DDD; 11-JUL-96.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein; 3D-structure.
FT   DOMAIN        1     41       EXTRACELLULAR (POTENTIAL).
```

```
FT   TRANSMEM     42     63       1 (POTENTIAL).
FT   DOMAIN       64     76       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     77     98       2 (POTENTIAL).
FT   DOMAIN       99    115       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    116    136       3 (POTENTIAL).
FT   DOMAIN      137    155       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    156    177       4 (POTENTIAL).
FT   DOMAIN      178    207       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    208    227       5 (POTENTIAL).
FT   DOMAIN      228    254       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    255    274       6 (POTENTIAL).
FT   DOMAIN      275    292       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    293    317       7 (POTENTIAL).
FT   DOMAIN      318    362       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    113    191       BY SIMILARITY.
FT   CARBOHYD     11     11       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    102    102       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   HELIX        42     69
FT   HELIX        77    102
FT   HELIX       115    137
FT   HELIX       154    178
FT   HELIX       205    231
FT   HELIX       250    275
FT   HELIX       290    305
FT   TURN        306    307
FT   HELIX       308    320
SQ   SEQUENCE   362 AA;  41194 MW;  A806C88FB9514761 CRC64;

  Query Match             28.6%;  Score 472.5;  DB 1;  Length 362;
  Best Local Similarity   35.9%;  Pred. No. 4.3e-25;
  Matches  110;  Conservative   58;  Mismatches  121;  Indels   17;  Gaps    8;

Qy          10 WLA----TEAILNK-----YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
               | |    |:  | |     |||   | : || | |||   :: ::| |: |:  :||:||
Db          22 WAAGNATTKCSLTKTGFQFYYLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMFN 81

Qy          61 LSISDFAFLCTLPILIKSYANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLL 119
               |:::|| :: ||| ||  | |     :|||:|   |:: | ||| |||||| ||: ||
Db          82 LALADFLYVLTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYTG 141

Qy         120 MKYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPE 178
               : :| :     ||: |: :|  |||||   : |:| :  : | : :   | |  :
Db         142 VVHPLKSLGRLKKKNAVYVSSLVWALVVAVIAPILFYSGTGVRRNKTITCYDTTADEYLR 201

Qy         179 HNLIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIF 237
                  :||:| |:  | ||  |:   |  :| |  :    :   ||  |   ||:: : :|
Db         202 SYFVYSMCTTVFMFCIPFIVILGCYGLIVKALIYKDLDNS---PLRRKSIYLVIIVLTVF 258

Qy         238 SILFTPYHIMRNLRIASRLD-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGD 295
               :: : |:|:|: | : :|||   || |     : : | :|| || ||| ::|| ||| ||
Db         259 AVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNSCVDPILYFLAGD 318

Qy         296 HYREML 301
                :|  |
Db         319 TFRRRL 324
```

```
RESULT 6
P2YR_MELGA
ID   P2YR_MELGA     STANDARD;      PRT;   362 AA.
AC   P49652;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   P2Y purinoceptor 1 (ATP receptor) (P2Y1) (Purinergic receptor) (6H1
DE   orphan receptor).
GN   P2RY1.
OS   Meleagris gallopavo (Common turkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX   NCBI_TaxID=9103;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=94335907; PubMed=8058061;
RA   Filtz T.M., Li Q., Boyer J.L., Nicholas R.A., Harden T.K.;
RT   "Expression of a cloned P2Y purinergic receptor that couples to
RT   phospholipase C.";
RL   Mol. Pharmacol. 46:8-14(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97382456; PubMed=9240460;
RA   Li Q., Schachter J.B., Harden T.K., Nicholas R.A.;
RT   "The 6H1 orphan receptor, claimed to be the p2y5 receptor, does not
RT   mediate nucleotide-promoted second messenger responses.";
RL   Biochem. Biophys. Res. Commun. 236:455-460(1997).
CC   -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADENINE NUCLEOTIDES SUCH AS
CC       ATP AND ADP. SEEMS TO MEDIATE ITS ACTION VIA A PERTUSSIS TOXIN
CC       INSENSITIVE G-PROTEIN, PROBABLY BELONGING TO THE GQ FAMILY THAT
CC       ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: MAINLY FOUND IN BLOOD, BRAIN, AND LUNG. TO A
CC       LESSER EXTENT IN STOMACH, GUT, AND SKELETAL MUSCLE.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U09842; AAA18784.1; -.
DR   EMBL; AF012103; AAB65428.1; -.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
```

```
FT   DOMAIN        1     41       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     42     63       1 (POTENTIAL).
FT   DOMAIN       64     76       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     77     98       2 (POTENTIAL).
FT   DOMAIN       99    115       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    116    136       3 (POTENTIAL).
FT   DOMAIN      137    155       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    156    177       4 (POTENTIAL).
FT   DOMAIN      178    207       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    208    227       5 (POTENTIAL).
FT   DOMAIN      228    254       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    255    274       6 (POTENTIAL).
FT   DOMAIN      275    292       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    293    317       7 (POTENTIAL).
FT   DOMAIN      318    362       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    113    191       BY SIMILARITY.
FT   CARBOHYD     11     11       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    102    102       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   362 AA;  41180 MW;  3E128AB9EB64349C CRC64;

  Query Match             28.6%;  Score 472.5;  DB 1;  Length 362;
  Best Local Similarity   35.9%;  Pred. No. 4.3e-25;
  Matches  110;  Conservative   58;  Mismatches  121;  Indels   17;  Gaps    8;

Qy          10 WLA----TEAILNK-----YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
               | |    |:  | |     |||   | : || | |||   :: ::| |: |:  :||:||
Db          22 WAAGNASTKCSLTKTGFQFYYLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMFN 81

Qy          61 LSISDFAFLCTLPILIKSYANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLL 119
               |:::|| :: ||| ||  | |     :|||:|   |:: | ||| ||||| ||: ||
Db          82 LALADFLYVLTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYTG 141

Qy         120 MKYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPE 178
               : :| :     ||: |: :|  |||||   : |:| :  : | : :   | |  :
Db         142 VVHPLKSLGRLKKKNAVYVSSLVWALVVAVIAPILFYSGTGVRRNKTITCYDTTADEYLR 201

Qy         179 HNLIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIF 237
                  :||:| |:  | ||  |:   |  :| |  :   :   ||  |   ||:: : :|
Db         202 SYFVYSMCTTVFMFCIPFIVILGCYGLIVKALIYKDLDNS---PLRRKSIYLVIIVLTVF 258

Qy         238 SILFTPYHIMRNLRIASRLD-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGD 295
               :: : |:|:|: | : :|||   || |     : : | :|| || ||| ::|| ||| ||
Db         259 AVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNSCVDPILYFLAGD 318

Qy         296 HYREML 301
                :|  |
Db         319 TFRRRL 324


RESULT 7
P2Y8_XENLA
ID   P2Y8_XENLA     STANDARD;      PRT;   537 AA.
AC   P79928;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
```

```
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   P2Y purinoceptor 8 (P2Y8).
GN   P2RY8.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Neural plate;
RX   MEDLINE=97284734; PubMed=9139711;
RA   Bogdanov Y.D., Dale L., King B.F., Whittock N., Burnstock G.;
RT   "Early expression of a novel nucleotide receptor in the neural plate
RT   of Xenopus embryos.";
RL   J. Biol. Chem. 272:12583-12590(1997).
CC   -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ATP, UTP, CTP, GTP AND ITP.
CC       THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC       ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC       MAY PLAY A KEY ROLE IN THE EARLY DEVELOPMENT OF NEURAL TISSUE.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X99953; CAA68213.1; -.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     49       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     50     70       1 (POTENTIAL).
FT   DOMAIN       71     79       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     80    100       2 (POTENTIAL).
FT   DOMAIN      101    118       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    119    139       3 (POTENTIAL).
FT   DOMAIN      140    161       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    162    182       4 (POTENTIAL).
FT   DOMAIN      183    210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    211    231       5 (POTENTIAL).
FT   DOMAIN      232    254       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    255    275       6 (POTENTIAL).
FT   DOMAIN      276    292       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    293    316       7 (POTENTIAL).
FT   DOMAIN      317    537       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    116    193       BY SIMILARITY.
FT   CARBOHYD     26     26       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     29     29       N-LINKED (GLCNAC. . .) (POTENTIAL).
```

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SQ   SEQUENCE   537 AA;  62024 MW;  B2CF24812F3C19F2 CRC64;

  Query Match             23.4%;  Score 386.5;  DB 1;  Length 537;
  Best Local Similarity   35.3%;  Pred. No. 3.6e-19;
  Matches  104;  Conservative   51;  Mismatches  125;  Indels   15;  Gaps    7;

Qy         22 LSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSYAN 81
              |   |:  |: ||  |:  :: ::  |: || : ||:|||::||  :: :|| |:  ||
Db         46 LPVSYSAVFMVGLPLNIAAMWIFIAKMRPWNPTTVYMFNLALSDTLYVLSLPTLVYYYA- 104

Qy         82 DKGT--YGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILIS 139
              ||    :|:|||   |:: : |||:|||||| ||: ||  : :|         : | :|
Db        105 DKNNWPFGEVLCKLVRFLFYANLYSSILFLTCISVHRYRGVCHPITSLRRMNAKHAYVIC 164

Qy        140 LAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
               ||  ||| ::| | |:   || : : | |     :    : ||  :  | | ||  ::
Db        165 ALVWLSVTLCLVPNLIFVTVSPKVKNTICHDTTRPEDFARYVEYSTAIMCLLFGIPCLII 224

Qy        200 CFFYYKMVVFLKRR--SQQQATALPLDKPQ--RLVVLAVVIFSILFTPYHIMRNLRIASR 255
                | |   | :   |  | | ||  | :  : ::  :: |:| | |:|| | |   :|
Db        225 AGCYGLMTRELMKPIVSGNQQT-LPSYKKRSIKTIIFVMIAFAICFMPFHITRTLYYYAR 283

Qy        256 LDSWPQGCTQKAIKSI---YTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQ 307
              |     |    |:  |   | :|||||  || |:|| |||  | ||  ||   |:
Db        284 L----LGIKCYALNVINVTYKVTRPLASANSCIDPILYFLANDRYRRRLIRTVRR 334


RESULT 8
P2Y3_CHICK
ID   P2Y3_CHICK     STANDARD;      PRT;   328 AA.
AC   Q98907;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   P2Y purinoceptor 3 (P2Y3) (Nucleoside diphosphate receptor).
GN   P2RY3.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96319774; PubMed=8700132;
RA   Webb T.E., Henderson D., King B.F., Wang S., Simon J.,
RA   Bateson A.N., Burnstock G., Barnard E.A.;
RT   "A novel G protein-coupled P2 purinoceptor (P2Y3) activated
RT   preferentially by nucleoside diphosphates.";
RL   Mol. Pharmacol. 50:258-265(1996).
CC   -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR ADP > UTP > ATP = UDP. THE
CC       ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC       A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; X98283; CAA66930.1; -.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     22       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     23     43       1 (POTENTIAL).
FT   DOMAIN       44     57       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     58     78       2 (POTENTIAL).
FT   DOMAIN       79     96       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     97    117       3 (POTENTIAL).
FT   DOMAIN      118    139       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    140    160       4 (POTENTIAL).
FT   DOMAIN      161    189       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    190    210       5 (POTENTIAL).
FT   DOMAIN      211    231       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    232    252       6 (POTENTIAL).
FT   DOMAIN      253    275       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    276    298       7 (POTENTIAL).
FT   DOMAIN      299    323       EXTRACELLULAR (POTENTIAL).
FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     94    172       BY SIMILARITY.
SQ   SEQUENCE   328 AA;  37586 MW;  7A3BF1C91F54FAAB CRC64;

  Query Match             23.0%;  Score 379.5;  DB 1;  Length 328;
  Best Local Similarity   29.6%;  Pred. No. 6.8e-19;
  Matches   88;  Conservative   63;  Mismatches  135;  Indels   11;  Gaps    4;

Qy         22 LSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSYA- 80
              |   |:: |: ||  |  |:       |    : :|: ||:::|  ::|:||:|| :|
Db         24 LPLVYSVVFLLGLPLNAVVIGQIWLARKALTRTTIYMLNLAMADLLYVCSLPLLIYNYTQ 83

Qy         81 NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFRE-HFLQKKEFAILIS 139
               |   :||  |   |:  :|||: |||||| ||: ||: : :|    |  : |:   |:
Db         84 KDYWPFGDFTCKFVRFQFYTNLHGSILFLTCISVQRYMGICHPLASWHKKKGKKLTWLVC 143

Qy        140 LAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
              ||| :|  : ||  | ::  :   : | | :          | : ||: |||:| : :
Db        144 AAVWFIVIAQCLPTFVFASTGTQRNRTVCYDLSPPDRSTSYFPYGITLTITGFLLPFAAI 203

Qy        200 CFFYYKMVVFLKRRSQQQATAL--PLDKPQRLVVLAVVIFSILFTPYHIMRNLRIASRLD 257
                |  |   | :: :    |:    ||  |:::: |::||| | |:|: : : :  |
Db        204 LACYCSMARILCQKDELIGLAVHKKKDKAVRMIIIVVIVFSISFFPFHLTKTIYLIVRSS 263

Qy        258 SWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE-------MLISKFRQ 307
              :    | :|    |  ||| | :|| ::|| ::     :||        : ||:||
Db        264 ASLPCPTLQAFAIAYKCTRPFASMNSVLDPILFYFTQRKFRESTRYLLDKMSSKWRQ 320
```

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RESULT 9
P2Y2_RAT
ID   P2Y2_RAT       STANDARD;      PRT;   374 AA.
AC   P41232;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)
DE   (Purinergic receptor).
GN   P2RY2 OR P2RU1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95110548; PubMed=7811468;
RA   Rice W.R., Burton F.M., Fiedeldey D.T.;
RT   "Cloning and expression of the alveolar type II cell P2u-purinergic
RT   receptor.";
RL   Am. J. Respir. Cell Mol. Biol. 12:27-32(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar; TISSUE=Pituitary;
RA   Chen Z.P., Krull N., Xu S., Levy A., Lightman S.L.;
RL   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wistar;
RX   MEDLINE=98099857; PubMed=9437211;
RA   Seye C.I., Gadeau A.P., Daret D., Dupuch F., Alzieu P., Capron L.,
RA   Desgranges C.;
RT   "Overexpression of P2Y2 purinoceptor in intimal lesions of the rat
RT   aorta.";
RL   Arterioscler. Thromb. Vasc. Biol. 17:3602-3610(1997).
CC   -!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
CC       activate a phosphatidylinositol-calcium second messenger system.
CC       The affinity range is UTP = ATP > ATP-gamma-S >> 2-methylthio-ATP
CC       = ADP.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U09402; AAA61565.1; -.
DR   EMBL; L46865; AAB02099.1; -.
DR   EMBL; U56839; AAC00048.1; -.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
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DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     32       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     33     59       1 (POTENTIAL).
FT   DOMAIN       60     70       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     71     93       2 (POTENTIAL).
FT   DOMAIN       94    110       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    111    129       3 (POTENTIAL).
FT   DOMAIN      130    152       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    153    172       4 (POTENTIAL).
FT   DOMAIN      173    194       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    195    220       5 (POTENTIAL).
FT   DOMAIN      221    245       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    246    268       6 (POTENTIAL).
FT   DOMAIN      269    286       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    287    308       7 (POTENTIAL).
FT   DOMAIN      309    374       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      9      9       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     13     13       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    106    183       BY SIMILARITY.
FT   CONFLICT    132    132       C -> S (IN REF. 1).
FT   CONFLICT    143    143       S -> R (IN REF. 1).
FT   CONFLICT    166    166       A -> T (IN REF. 1).
FT   CONFLICT    188    188       A -> D (IN REF. 1).
SQ   SEQUENCE   374 AA;  42137 MW;  2DA6853AA20A1AF3 CRC64;

  Query Match             22.7%;  Score 374;  DB 1;  Length 374;
  Best Local Similarity   33.8%;  Pred. No. 1.8e-18;
  Matches   96;  Conservative   50;  Mismatches  124;  Indels   14;  Gaps    7;

Qy         19 KY-YLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIK 77
              ||  |   | :  : ||  ||  :: :|  :| ||:|  |:|:|::||  :  :||:|:
Db         32 KYVLLPVSYGVVCVLGLCLNVVALYIFLCRLKTWNASTTYMFHLAVSDSLYAASLPLLVY 91

Qy         78 SYA-NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAI 136
               ||  |   :  |||   |:: :|||| |||||| ||: | | :  |          :|
Db         92 YYAQGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLHSLSWGHARYAR 151

Qy        137 LISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPL 196
              ::  || ||     |:| |: :  :     | | ::     | : ||  :  | | :|
Db        152 RVAAVVWVLVLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSSVMLGLLFAVPF 211

Qy        197 SVMCFFYYKMVVFLKRRSQQQA---TALPLDKPQ--RLVVLAVVIFSILFTPYHIMRNLR 251
              |::   |    | : ||  : |   | ||  | :  | : | : :|:: | |:|: | |
Db        212 SIILVCY----VLMARRLLKPAYGTTGLPRAKRKSVRTIALVLAVFALCFLPFHVTRTLY 267

Qy        252 IASRLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMG 294
              : |  |    | |  ||   | :|||||  || ::|: ||| |
Db        268 YSFR--SLDLSCHTLNAINMAYKITRPLASANSCLDPVLYFLAG 309


RESULT 10
P2Y2_MOUSE
ID   P2Y2_MOUSE     STANDARD;      PRT;   373 AA.
```

AC   P35383; O09031; Q9CPZ4;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)
DE   (Purinergic receptor).
GN   P2RY2 OR P2RU1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93281707; PubMed=7685114;
RA   Lustig K.D., Shiau A.K., Brake A.J., Julius D.;
RT   "Expression cloning of an ATP receptor from mouse neuroblastoma
RT   cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 90:5113-5117(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96316177; PubMed=8739319;
RA   Enomoto K., Furuya K., Moore R.C., Yamagishi S., Oka T., Maeno T.;
RT   "Expression cloning and signal transduction pathway of P2U receptor
RT   in mammary tumor cells.";
RL   Biol. Signals 5:9-21(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Head, and Liver;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

```
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   MUTAGENESIS OF LYS-107; ARG-110; HIS-262; ARG-265; LYS-289 AND
RP   ARG-292.
RX   MEDLINE=95181393; PubMed=7876172;
RA   Erb L., Garrad R.C., Wang Y., Quinn T., Turner J.T., Weisman G.A.;
RT   "Site-directed mutagenesis of P2U purinoceptors. Positively charged
RT   amino acids in transmembrane helices 6 and 7 affect agonist potency
RT   and specificity.";
RL   J. Biol. Chem. 270:4185-4188(1995).
CC   -!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
CC       activate a phosphatidylinositol-calcium second messenger system.
CC       The affinity range is UTP = ATP > ATP-gamma-S >> 2-methylthio-ATP
CC       = ADP.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: SPLEEN, TESTIS, KIDNEY, LIVER, LUNG, HEART AND
CC       BRAIN.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L14751; AAA39871.1; -.
DR   EMBL; S83099; AAB50735.1; -.
DR   EMBL; AK005013; BAB23746.1; -.
DR   EMBL; AK017378; BAB30719.1; -.
DR   EMBL; BC006613; AAH06613.1; -.
DR   PIR; A47556; A47556.
DR   HSSP; P34996; 1DDD.
DR   MGD; MGI:105107; P2ry2.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     32       EXTRACELLULAR (POTENTIAL).
```

```
FT   TRANSMEM     33     59       1 (POTENTIAL).
FT   DOMAIN       60     70       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     71     93       2 (POTENTIAL).
FT   DOMAIN       94    110       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    111    129       3 (POTENTIAL).
FT   DOMAIN      130    152       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    153    172       4 (POTENTIAL).
FT   DOMAIN      173    194       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    195    220       5 (POTENTIAL).
FT   DOMAIN      221    246       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    247    269       6 (POTENTIAL).
FT   DOMAIN      270    287       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    288    309       7 (POTENTIAL).
FT   DOMAIN      310    373       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      9      9       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     13     13       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    106    183       BY SIMILARITY.
FT   MUTAGEN     107    107       K->I: NO EFFECT ON RECEPTOR ACTIVATION.
FT   MUTAGEN     110    110       R->L: NO EFFECT ON RECEPTOR ACTIVATION.
FT   MUTAGEN     262    262       H->L: DECREASE IN RECEPTOR ACTIVATION.
FT   MUTAGEN     265    265       R->L: DECREASE IN RECEPTOR ACTIVATION.
FT   MUTAGEN     289    289       K->I: NO EFFECT ON RECEPTOR ACTIVATION.
FT   MUTAGEN     292    292       R->L: DECREASE IN RECEPTOR ACTIVATION.
FT   CONFLICT     17     17       E -> D (IN REF. 2).
FT   CONFLICT    120    120       S -> R (IN REF. 2).
FT   CONFLICT    125    125       T -> N (IN REF. 2).
FT   CONFLICT    196    196       V -> M (IN REF. 2).
FT   CONFLICT    263    263       V -> L (IN REF. 3).
FT   CONFLICT    355    355       D -> N (IN REF. 2).
FT   CONFLICT    369    371       KDI -> PYV (IN REF. 2).
SQ   SEQUENCE   373 AA;  42174 MW;  590BBE502E41B3AE CRC64;
```

```
  Query Match             22.6%;  Score 373.5;  DB 1;  Length 373;
  Best Local Similarity   33.5%;  Pred. No. 1.9e-18;
  Matches   94;  Conservative   50;  Mismatches  130;  Indels    7;  Gaps    5;

Qy          19 KY-YLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIK 77
               ||  |   | :  : ||  ||  :: :|  :| ||:|  |:|:|::||  :  :|||:|:
Db          32 KYVLLPVSYGVVCVLGLCLNVVALYIFLCRLKTWNASTTYMFHLAVSDSLYAASLPLLVY 91

Qy          78 SYA-NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAI 136
                ||  |   :  |||   |:: :|||| |||||| ||: | | :  |       :  :|
Db          92 YYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLHSLRWGRARYAR 151

Qy         137 LISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPL 196
                ::  || ||     |:| |: :  :     | | ::     | : ||  :  | | :|
Db         152 RVAAVVWVLVLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSSVMLGLLFAVPF 211

Qy         197 SVMCFFYYKMVVFLKRRSQQQATALPLDKPQ--RLVVLAVVIFSILFTPYHIMRNLRIAS 254
               ||:   |  |   | : :      ||  | :  | : | : :|:: | |:|: | |  :
Db         212 SVILVCYVLMARRLLKPAYGTTGGLPRAKRKSVRTIALVLAVFALCFLPFHVTRTLYYSF 271

Qy         255 RLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMG 294
               |  |    | |  ||   | :|||||  || ::|: ||| |
Db         272 R--SLDLSCHTLNAINMAYKITRPLASANSCLDPVLYFLAG 310
```

```
RESULT 11
P2Y3_MELGA
ID   P2Y3_MELGA     STANDARD;      PRT;   328 AA.
AC   O93361;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   P2Y purinoceptor 3 (P2Y3) (Nucleoside diphosphate receptor).
GN   P2RY3.
OS   Meleagris gallopavo (Common turkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX   NCBI_TaxID=9103;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98401046; PubMed=9730913;
RA   Li Q., Olesky M., Palmer R.K., Harden T.K., Nicholas R.A.;
RT   "Evidence that the p2y3 receptor is the avian homologue of the
RT   mammalian P2Y6 receptor.";
RL   Mol. Pharmacol. 54:541-546(1998).
CC   -!- FUNCTION: RECEPTOR FOR EXTRACELLULAR UDP> ADP = UTP. THE ACTIVITY
CC       OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE A
CC       PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF069555; AAC23863.1; -.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     22       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     23     43       1 (POTENTIAL).
FT   DOMAIN       44     57       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     58     78       2 (POTENTIAL).
FT   DOMAIN       79     96       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     97    117       3 (POTENTIAL).
FT   DOMAIN      118    139       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    140    160       4 (POTENTIAL).
FT   DOMAIN      161    189       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    190    210       5 (POTENTIAL).
FT   DOMAIN      211    231       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    232    252       6 (POTENTIAL).
FT   DOMAIN      253    275       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    276    298       7 (POTENTIAL).
FT   DOMAIN      299    323       EXTRACELLULAR (POTENTIAL).
```

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FT   CARBOHYD      5      5       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID     94    172       BY SIMILARITY.
SQ   SEQUENCE   328 AA;  37594 MW;  B74D49B99C7164A5 CRC64;

  Query Match             22.5%;  Score 371.5;  DB 1;  Length 328;
  Best Local Similarity   29.4%;  Pred. No. 2.3e-18;
  Matches   87;  Conservative   61;  Mismatches  137;  Indels   11;  Gaps    4;

Qy         22 LSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSYA- 80
              |   |:: |: ||  |  |:       |    : :|: ||: :|  ::|:||:|| :|
Db         24 LPLVYSVVFLLGLPLNAVVIGQIWLARKALTRTTIYMLNLATADLLYVCSLPLLIYNYTQ 83

Qy         81 NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFRE-HFLQKKEFAILIS 139
               |   :||  |   |:  :|||: |||||| ||: ||: : :|    |  : |:   |:
Db         84 KDYWPFGDFTCKFVRFQFYTNLHGSILFLTCISVQRYMGICHPLASWHKKKGKKLTWLVC 143

Qy        140 LAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
              ||| :|  : ||   | ::  :   : | | :          | : ||: |||:| : :
Db        144 AAVWFIVIAQCLPTFVFASTGTQRNRTVCYDLSPPDRSASYFPYGITLTITGFLLPFAAI 203

Qy        200 CFFYYKMVVFLKRRSQQQATAL--PLDKPQRLVVLAVVIFSILFTPYHIMRNLRIASRLD 257
                |  |   | :: :    |:    ||  |:::: |::||| | |:|: : : :  |
Db        204 LACYCSMARILCQKDELIGLAVHKKKDKAVRMIIIVVIVFSISFFPFHLTKTIYLIVRSS 263

Qy        258 SWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYRE-------MLISKFR 306
                  | :|    |  ||| | :|| ::|| ::     :||        : ||:|
Db        264 PTLPCPTLQAFAIAYKCTRPFASMNSVLDPILFYFTQRKFRESTRYLLDKMSSKWR 319


RESULT 12
P2Y2_HUMAN
ID   P2Y2_HUMAN     STANDARD;      PRT;   377 AA.
AC   P41231; Q96EM8;
DT   01-FEB-1995 (Rel. 31, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)
DE   (Purinergic receptor).
GN   P2RY2 OR P2RU1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Airway epithelium;
RX   MEDLINE=94211846; PubMed=8159738;
RA   Parr C.E., Sullivan D.M., Paradiso A.M., Lazarowski E.R., Burch L.H.,
RA   Olsen J.C., Erb L., Weisman G.A., Boucher R.C., Turner J.T.;
RT   "Cloning and expression of a human P2U nucleotide receptor, a target
RT   for cystic fibrosis pharmacotherapy.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:3275-3279(1994).
RN   [2]
RP   REVISIONS.
RX   MEDLINE=95108098; PubMed=7809171;
RA   Parr C.E., Sullivan D.M., Paradiso A.M., Lazarowski E.R., Burch L.H.,
RA   Olsen J.C., Erb L., Weisman G.A., Boucher R.C., Turner J.T.;
```

```
RT   "Cloning and expression of a human P2U nucleotide receptor, a target
RT   for cystic fibrosis pharmacotherapy.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:13067-13067(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney, and Leukocyte;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
CC       activate a phosphatidylinositol-calcium second messenger system.
CC       The affinity range is UTP = ATP > ATP-gamma-S >> 2-methylthio-ATP
CC       = ADP.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: SPLEEN, TESTIS, KIDNEY, LIVER, LUNG, HEART AND
CC       BRAIN.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U07225; AAC04923.1; -.
DR   EMBL; BC012104; AAH12104.1; -.
DR   EMBL; BC028135; AAH28135.1; -.
DR   HSSP; P34996; 1DDD.
DR   Genew; HGNC:8541; P2RY2.
DR   MIM; 600041; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   GO; GO:0006873; P:cell ion homeostasis; TAS.
DR   GO; GO:0007200; P:G-protein signaling, coupled to IP3 second . . .; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
```

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DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     32       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     33     59       1 (POTENTIAL).
FT   DOMAIN       60     70       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     71     93       2 (POTENTIAL).
FT   DOMAIN       94    110       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    111    129       3 (POTENTIAL).
FT   DOMAIN      130    152       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    153    172       4 (POTENTIAL).
FT   DOMAIN      173    194       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    195    220       5 (POTENTIAL).
FT   DOMAIN      221    246       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    247    269       6 (POTENTIAL).
FT   DOMAIN      270    287       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    288    309       7 (POTENTIAL).
FT   DOMAIN      310    377       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD      9      9       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     13     13       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    106    183       BY SIMILARITY.
FT   CONFLICT    312    312       R -> S (IN REF. 3; AAH12104).
FT   CONFLICT    350    350       E -> G (IN REF. 1).
FT   CONFLICT    359    359       S -> F (IN REF. 1).
SQ   SEQUENCE   377 AA;  42289 MW;  EE557A857A269AC6 CRC64;

  Query Match             22.0%;  Score 363.5;  DB 1;  Length 377;
  Best Local Similarity   33.5%;  Pred. No. 9.1e-18;
  Matches   94;  Conservative   52;  Mismatches  128;  Indels    7;  Gaps    5;

Qy         19 KY-YLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIK 77
              ||  |   | :  : ||  |   :: :|  :| ||:|  |:|:|::||  :  :||:|:
Db         32 KYVLLPVSYGVVCVLGLCLNAVALYIFLCRLKTWNASTTYMFHLAVSDALYAASLPLLVY 91

Qy         78 SYA-NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAI 136
               ||  |   :  |||   |:: :|||| |||||| ||: | | :  | |     :  :|
Db         92 YYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLRSLRWGRARYAR 151

Qy        137 LISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPL 196
               :: ||| ||     |:| |: :  :     | | ::       : ||  :  | | :|
Db        152 RVAGAVWVLVLACQAPVLYFVTTSARGGRVTCHDTSAPELFSRFVAYSSVMLGLLFAVPF 211

Qy        197 SVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVV--IFSILFTPYHIMRNLRIAS 254
               :|:   |  |   | : :   :  ||  | : :  :|||  :|:: | |:|: | |  :
Db        212 AVILVCYVLMARRLLKPAYGTSGGLPRAKRKSVRTIAVVLAVFALCFLPFHVTRTLYYSF 271

Qy        255 RLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMG 294
               |  |    | |  ||   | :|||||  || ::|: ||| |
Db        272 R--SLDLSCHTLNAINMAYKVTRPLASANSCLDPVLYFLAG 310


RESULT 13
P2Y4_RAT
ID   P2Y4_RAT       STANDARD;      PRT;   361 AA.
AC   O35811;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
```

```
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   P2Y purinoceptor 4 (P2Y4).
GN   P2RY4 OR P2Y4.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Liver;
RA   Bogdanov Y.D., Wildman S., King B.F., Burntock G.;
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=98421785; PubMed=9751165;
RA   Webb T.E., Henderson D., Roberts J.A., Barnard E.A.;
RT   "Molecular cloning and characterization of the rat P2Y4 receptor.";
RL   J. Neurochem. 71:1424-1434(1998).
CC   -!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
CC       activate a phosphatidylinositol-calcium second messenger system.
CC       Not activated by ADP or UDP.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Widely expressed at low levels. In brain,
CC       higher expression in the pineal gland and ventricular system.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Y14705; CAA75007.1; -.
DR   EMBL; Y11433; CAA72241.1; -.
DR   HSSP; P34996; 1DDD.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     30       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     31     58       1 (POTENTIAL).
FT   DOMAIN       59     68       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     69     91       2 (POTENTIAL).
FT   DOMAIN       92    108       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    109    127       3 (POTENTIAL).
FT   DOMAIN      128    149       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    150    170       4 (POTENTIAL).
FT   DOMAIN      171    192       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    193    218       5 (POTENTIAL).
FT   DOMAIN      219    242       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    243    265       6 (POTENTIAL).
FT   DOMAIN      266    283       EXTRACELLULAR (POTENTIAL).
```

```
FT   TRANSMEM    284    305       7 (POTENTIAL).
FT   DOMAIN      306    361       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    104    181       BY SIMILARITY.
FT   CARBOHYD    175    175       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   361 AA;  40893 MW;  0377F96E54B449A3 CRC64;

  Query Match             21.5%;  Score 354;  DB 1;  Length 361;
  Best Local Similarity   30.6%;  Pred. No. 3.8e-17;
  Matches   86;  Conservative   60;  Mismatches  125;  Indels   10;  Gaps    5;

Qy         26 YAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY-ANDKG 84
              ||: |: ||  |   :: :|| :: |:::  |:|:|::||  :: :|| |:  | | :
Db         38 YAVVFVLGLALNAPTLWLFLFRLRPWDATATYMFHLALSDTLYVLSLPTLVYYYAARNHW 97

Qy         85 TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILISLAVWA 144
               :|  ||   |:: : ||| |:|||| ||: ||| : :| |     :  || |: | ||
Db         98 PFGTGLCKFVRFLFYWNLYCSVLFLTCISVHRYLGICHPLRAIRWGRPRFASLLCLGVWL 157

Qy        145 LVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVMCFFYY 204
               :|   ::| | |: :         | |       :| : :|  : :| | :|  :    |
Db        158 VVAGCLVPNLFFVTTNANGTTILCHDTTLPEEFDHYVYFSSAVMVLLFGLPFLITLVCYG 217

Qy        205 KMVVFLKR---RSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIASRLDSWPQ 261
              |   | |    : | :: |   :  | : : : :|:: | |:|| | :   :||
Db        218 LMARRLYRPLPGAGQSSSRL----RSLRTIAVVLTVFAVCFVPFHITRTIYYQARL--LQA 272

Qy        262 GC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
              |     :  :| :|||||  || ::|: |   || ||  |
Db        273 DCHVLNIVNVVYKVTRPLASANSCLDPVLYLFTGDKYRNQL 313


RESULT 14
C3X1_HUMAN
ID   C3X1_HUMAN     STANDARD;      PRT;   355 AA.
AC   P49238;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   CX3C chemokine receptor 1 (C-X3-C CKR-1) (CX3CR1) (Fractalkine
DE   receptor) (GPR13) (V28) (Beta chemokine receptor-like 1) (CMK-BRL-1)
DE   (CMKBLR1).
GN   CX3CR1 OR GPR13.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96011651; PubMed=7590284;
RA   Raport C.J., Schweickart V.L., Eddy R.L. Jr., Shows T.B., Gray P.W.;
RT   "The orphan G-protein-coupled receptor-encoding gene V28 is closely
RT   related to genes for chemokine receptors and is expressed in lymphoid
RT   and neural tissues.";
RL   Gene 163:295-299(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95374679; PubMed=7646814;
```

```
RA   Combadiere C., Ahuja S.K., Murphy P.M.;
RT   "Cloning, chromosomal localization, and RNA expression of a human
RT   beta chemokine receptor-like gene.";
RL   DNA Cell Biol. 14:673-680(1995).
RN   [3]
RP   CHARACTERIZATION.
RX   MEDLINE=98050927; PubMed=9390561;
RA   Imai T., Hieshima K., Haskell C., Baba M., Nagira M., Nishimura M.,
RA   Kakizaki M., Takagi S., Nomiyama H., Schall T.J., Yoshie O.;
RT   "Identification and molecular characterization of fractalkine receptor
RT   CX3CR1, which mediates both leukocyte migration and adhesion.";
RL   Cell 91:521-530(1997).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=98395093; PubMed=9726990;
RA   Combadiere C., Salzwedel K., Smith E.D., Tiffany H.L., Berger E.A.,
RA   Murphy P.M.;
RT   "Identification of CX3CR1. A chemotactic receptor for the human CX3C
RT   chemokine fractalkine and a fusion coreceptor for HIV-1.";
RL   J. Biol. Chem. 273:23799-23804(1998).
RN   [5]
RP   VARIANTS ALA-57; ILE-122; ILE-249 AND MET-280.
RX   MEDLINE=20196025; PubMed=10731151;
RA   Faure S., Meyer L., Costagliola D., Vaneensberghe C., Genin E.,
RA   Autran B., Delfraissy J.-F., McDermott D.H., Murphy P.M., Debre P.,
RA   Theodorou I., Combadiere C.;
RT   "Rapid progression to AIDS in HIV+ individuals with a structural
RT   variant of the chemokine receptor CX3CR1.";
RL   Science 287:2274-2277(2000).
CC   -!- FUNCTION: RECEPTOR FOR THE CX3C CHEMOKINE FRACTALKINE AND MEDIATES
CC       BOTH ITS ADHESIVE AND MIGRATORY FUNCTIONS. ACTS AS CO-RECEPTOR
CC       WITH CD4 FOR HIV-1 VIRUS ENVELOPE PROTEIN (IN VITRO).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID AND NEURAL TISSUES.
CC   -!- DISEASE: INCREASED SUSCEPTIBILITY TO HIV INFECTION AND RAPID
CC       PROGRESSION TO AIDS ARE ASSOCIATED WITH THE I-249/M-280 HAPLOTYPE.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U20350; AAA91783.1; -.
DR   EMBL; U28934; AAA87032.1; -.
DR   PIR; JC4304; JC4304.
DR   Genew; HGNC:2558; CX3CR1.
DR   MIM; 601470; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004950; F:chemokine receptor activity; TAS.
DR   GO; GO:0007155; P:cell adhesion; TAS.
DR   GO; GO:0006968; P:cellular defense response; TAS.
DR   GO; GO:0006935; P:chemotaxis; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
```

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DR   InterPro; IPR005387; Fractalkiner.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR01562; FRACTALKINER.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Polymorphism.
FT   DOMAIN        1     31       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     32     59       1 (POTENTIAL).
FT   DOMAIN       60     69       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     70     90       2 (POTENTIAL).
FT   DOMAIN       91    103       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    104    125       3 (POTENTIAL).
FT   DOMAIN      126    142       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    143    167       4 (POTENTIAL).
FT   DOMAIN      168    195       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    196    215       5 (POTENTIAL).
FT   DOMAIN      216    231       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    232    256       6 (POTENTIAL).
FT   DOMAIN      257    273       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    274    297       7 (POTENTIAL).
FT   DOMAIN      298    355       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    102    175       BY SIMILARITY.
FT   VARIANT      57     57       T -> A.
FT                                /FTId=VAR_010041.
FT   VARIANT     122    122       V -> I.
FT                                /FTId=VAR_010042.
FT   VARIANT     249    249       V -> I (COMMON POLYMORPHISM IN CAUCASIAN
FT                                POPULATION).
FT                                /FTId=VAR_010043.
FT   VARIANT     280    280       T -> M (COMMON POLYMORPHISM IN CAUCASIAN
FT                                POPULATION).
FT                                /FTId=VAR_010044.
SQ   SEQUENCE   355 AA;  40396 MW;  C59DC5F4C4312F22 CRC64;

  Query Match             21.4%;  Score 353;  DB 1;  Length 355;
  Best Local Similarity   28.1%;  Pred. No. 4.4e-17;
  Matches   84;  Conservative   66;  Mismatches  133;  Indels   16;  Gaps    6;

Qy         16 ILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPIL 75
              :    :|| ||:: |  ||:||: |||      |  : :::|| ||::||  |: |||
Db         28 VFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSDLLFVATLPFW 87

Qy         76 IKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA 135
                   |:|| : : :|          : || |:| ||:|||| :         :  :
Db         88 THYLINEKGLH-NAMCKFTTAFFFIGFFGSIFFITVISIDRYLAIVLAANSMNNRTVQHG 146

Qy        136 ILISLAVWALVTLEVLPMLTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLI 194
              : ||| |||   |   |   |     |:: : |: ||         :: ::    ||||:
Db        147 VTISLGVWAAAILVAAPQFMF----TKQKENECLGDYPEVLQEIWPVLRNVETNFLGFLL 202

Qy        195 PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIA 253
              || :| : |:::      :: ::| |:      :|::| |::| : :|||::|  |
Db        203 PLLIMSYCYFRIIQTLFSCKNHKKAKAI------KLILLVVIVFFLFWTPYNVMIFLETL 256

Qy        254 SRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
```

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                  | :|    :| ::   ::|  :|| :  :||: |   |: :|  |   :  | | |
Db        257 KLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYL---YHLYGKCL 312


RESULT 15
P2Y4_HUMAN
ID   P2Y4_HUMAN     STANDARD;      PRT;   365 AA.
AC   P51582;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   P2Y purinoceptor 4 (P2Y4) (Uridine nucleotide receptor) (UNR) (P2P).
GN   P2RY4 OR NRU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96125055; PubMed=8537336;
RA   Communi D., Pirotton S., Parmentier M., Boeynaems J.-M.;
RT   "Cloning and functional expression of a human uridine nucleotide
RT   receptor.";
RL   J. Biol. Chem. 270:30849-30852(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96125054; PubMed=8537335;
RA   Nguyen T., Erb L., Weisman G.A., Marchese A., Heng H.H.Q.,
RA   Garrad R.C., George S.R., Turner J.T., O'Dowd B.F.;
RT   "Cloning, expression, and chromosomal localization of the human
RT   uridine nucleotide receptor gene.";
RL   J. Biol. Chem. 270:30845-30848(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pancreas;
RX   MEDLINE=96197801; PubMed=8617367;
RA   Stam N.J., Klomp J., van der Heuvel M., Olijve W.;
RT   "Molecular cloning and characterization of a novel orphan receptor
RT   (P2P) expressed in human pancreas that shows high structural homology
RT   to the P2U purinoceptor.";
RL   FEBS Lett. 384:260-264(1996).
CC   -!- FUNCTION: Receptor for UTP and UDP coupled to G-proteins that
CC       activate a phosphatidylinositol-calcium second messenger system.
CC       Not activated by ATP or ADP.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Pancreas.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X91852; CAA62963.1; -.
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DR   EMBL; U40223; AAC50347.1; -.
DR   EMBL; X96597; CAA65415.1; -.
DR   PIR; S68679; S68679.
DR   HSSP; P34996; 1DDD.
DR   Genew; HGNC:8542; P2RY4.
DR   MIM; 300038; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0015065; F:uridine nucleotide receptor activity; TAS.
DR   GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Polymorphism.
FT   DOMAIN        1     34       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     35     61       1 (POTENTIAL).
FT   DOMAIN       62     72       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     73     95       2 (POTENTIAL).
FT   DOMAIN       96    112       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    113    131       3 (POTENTIAL).
FT   DOMAIN      132    154       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    155    174       4 (POTENTIAL).
FT   DOMAIN      175    196       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    197    222       5 (POTENTIAL).
FT   DOMAIN      223    246       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    247    269       6 (POTENTIAL).
FT   DOMAIN      270    287       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    288    309       7 (POTENTIAL).
FT   DOMAIN      310    365       CYTOPLASMIC (POTENTIAL).
FT   DISULFID    108    185       BY SIMILARITY.
FT   VARIANT     168    168       V -> M (IN dbSNP:1152186).
FT                                /FTId=VAR_011854.
FT   VARIANT     178    178       N -> T (IN dbSNP:1152187).
FT                                /FTId=VAR_011855.
FT   VARIANT     191    191       P -> L (IN dbSNP:1152188).
FT                                /FTId=VAR_011856.
FT   CONFLICT     86     86       L -> V (IN REF. 2).
FT   CONFLICT    234    234       S -> A (IN REF. 2).
SQ   SEQUENCE   365 AA;  40963 MW;  23E0AFED3B7BDEED CRC64;

  Query Match             21.3%;  Score 352;  DB 1;  Length 365;
  Best Local Similarity   31.1%;  Pred. No. 5.2e-17;
  Matches   90;  Conservative   59;  Mismatches  122;  Indels   18;  Gaps    6;

Qy         22 LSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY-A 80
              |   ||: |: ||  |   :: ::| :: |::: |:|:|::||  :: :|| ||  | |
Db         38 LPVSYAVVFVLGLGLNAPTLWLFIFRLRPWDATATYMFHLALSDTLYVLSLPTLIYYYAA 97

Qy         81 NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILISL 140
              ::   :|  :|   |:: : ||| |:|||| ||: ||| : :| |     :   | |: |
Db         98 HNHWPFGTEICKFVRFLFYWNLYCSVLFLTCISVHRYLGICHPLRALRWGRPRLAGLLCL 157

Qy        141 AVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVMC 200
              ||| :|   ::| | |: :  |     | |       :| : :|  :  | | :|  |
Db        158 AVWLVVAGCLVPNLFFVTTSNKGTTVLCHDTTRPEEFDHYVHFSSAVMGLLFGVPCLVTL 217
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```
Qy        201 FFYYKMVVFLKRR--------SQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIA 253
                |  |     ||       | | :: |   :  | : : : :|:: | |:|| | :
Db        218 VCYGLMA-----RRLYQPLPGSAQSSSRL---RSLRTIAVVLTVFAVCFVPFHITRTIYYL 270

Qy        254 SRLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
              :||       |    :  :| :|||||  || ::|: | | || ||  |
Db        271 ARL--LEADCRVLNIVNVVYKVTRPLASANSCLDPVLYLLTGDKYRRQL 317
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Search completed: December 12, 2003, 18:07:38
Job time : 19 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: December 12, 2003, 18:05:17 ; Search time 20 Seconds
(without alignments)
1524.274 Million cell updates/sec

Title: US-09-891-138A-2
Perfect score: 1650
Sequence: 1 MAQNLSCENWLATEAILNKY.....REMLISKFRQYFKSLTSFRT 317

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	474	28.7	373	2	JC4162	P2Y receptor - bov
2	474	28.7	373	2	JC4737	G protein-coupled
3	472.5	28.6	362	2	S33733	G protein-coupled
4	373.5	22.6	373	2	A47556	ATP receptor P2u -
5	353	21.4	355	2	JC4304	orphan G protein-c
6	352	21.3	365	2	S68679	G protein-coupled
7	336.5	20.4	360	2	A57160	chemokine (C-C) re
8	336	20.4	328	2	I55450	G protein-coupled
9	335.5	20.3	375	2	A54946	P-2U nucleotide re
10	333	20.2	308	2	I50241	G protein-coupled
11	332.5	20.2	354	2	I58186	probable G protein
12	332	20.1	328	2	JC4800	P2Y6 receptor - hu
13	328	19.9	355	2	A45177	chemokine (C-C) re

14	326.5	19.8	360	2	JC4587	chemokine (C-C) re
15	325.5	19.7	388	2	JN0605	somatostatin recep
16	318.5	19.3	359	2	A48921	interleukin-8 rece
17	317.5	19.2	355	2	A55733	G protein-coupled
18	316.5	19.2	384	2	A47249	brain-specific som
19	315.5	19.1	355	2	JQ1231	interleukin-8 rece
20	315	19.1	355	2	JC5067	G protein-coupled
21	314	19.0	369	2	JC2083	somatostatin recep
22	314	19.0	369	2	B41795	somatostatin recep
23	314	19.0	370	2	JC5549	heptahelical P2Y5-
24	313	19.0	344	2	T09508	intron 17 purinerg
25	312.5	18.9	360	2	A53611	interleukin-8 rece
26	311	18.8	358	2	A53752	interleukin-8 rece
27	309.5	18.8	384	2	JC4629	somatostatin recep
28	309	18.7	355	2	I49339	macrophage inflamm
29	308	18.7	369	2	D41795	somatostatin recep
30	307.5	18.6	369	2	A45291	somatostatin recep
31	306	18.5	356	2	I49340	MIP-1 alpha recept
32	306	18.5	362	2	A39714	G protein-coupled
33	306	18.5	391	2	A39297	somatostatin recep
34	305	18.5	346	2	S29248	somatostatin recep
35	304.5	18.5	361	2	B45680	G protein-coupled
36	303	18.4	350	2	A39445	interleukin-8 rece
37	303	18.4	391	2	A41795	somatostatin recep
38	303	18.4	391	2	C41795	somatostatin recep
39	302	18.3	366	1	OORTB2	bradykinin recepto
40	301.5	18.3	369	2	JC5068	G protein-coupled
41	301	18.2	355	2	G02436	chemokine (C-C) re
42	299.5	18.2	353	2	A53858	bradykinin recepto
43	298	18.1	354	2	T09353	G protein-coupled
44	297	18.0	387	2	I69202	G protein-coupled
45	295.5	17.9	363	2	I57955	somatostatin recep

ALIGNMENTS

RESULT 1
JC4162
P2Y receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 24-Sep-1999
C;Accession: JC4162
R;Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
Biochem. Biophys. Res. Commun. 212, 648-656, 1995
A;Title: Cloning and characterisation of a bovine P2Y receptor.
A;Reference number: JC4162; MUID:95352058; PMID:7626079
A;Accession: JC4162
A;Molecule type: mRNA
A;Residues: 1-373 <HEN>
A;Cross-references: EMBL:X87628; NID:g1032484; PIDN:CAA60958.1; PID:g1032485
A;Experimental source: aortic endothelial cell
C;Genetics:
A;Gene: bovp2y
C;Superfamily: ATP receptor P2u
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F;52-77/Domain: transmembrane #status predicted <TM1>

F;88-111/Domain: transmembrane #status predicted <TM2>
F;124-150/Domain: transmembrane #status predicted <TM3>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 28.7%; Score 474; DB 2; Length 373;
Best Local Similarity 36.6%; Pred. No. 4e-32;
Matches 105; Conservative 58; Mismatches 116; Indels 8; Gaps 6;

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Qy         20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
              ||| | | : || | |||   :: ::| || |:  :||:|||:::|| :: ||| ||  |
Db         52 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 111

Qy         80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
               |     :|| :|   |:: | ||| |||||| ||  ||  : || :     ||: |: |
Db        112 FNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAVYI 171

Qy        139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
              |: || :| : : |:| :  : : | :   | |  |         |||:| |:  | :||
Db        172 SVLVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSMCTTVAMFCVPLV 231

Qy        198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
              ::   | :|  |  :    :   ||  |   ||:: : :|:: : |:|:|: : : :||
Db        232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 288

Qy        257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
              |   |: |     : : | :|| || ||| ::|| ||| || :|  |
Db        289 DFQTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335
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RESULT 2
JC4737
G protein-coupled receptor P2Y1 - human
N;Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000
C;Accession: JC4737; JC4615; S54253
R;Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 221, 588-593, 1996
A;Title: Cloning and tissue distribution of the human P2Y1 receptor.
A;Reference number: JC4737; MUID:96205320; PMID:8630005
A;Accession: JC4737
A;Molecule type: DNA
A;Residues: 1-373 <JAN>
A;Cross-references: GB:S81950; NID:g1839438; PIDN:AAB47091.1; PID:g1839439
R;Ayyanathan, K.; Webbs, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, S.P.
Biochem. Biophys. Res. Commun. 218, 783-788, 1996
A;Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.
A;Reference number: JC4615; MUID:96158962; PMID:8579591
A;Accession: JC4615

A;Molecule type: mRNA
A;Residues: 1-373 <AYY>
A;Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731
A;Experimental source: erythro leukemia cells
R;Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.
submitted to the EMBL Data Library, May 1995
A;Description: Cloning of a human putative P2Y receptor.
A;Reference number: S54253
A;Accession: S54253
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137,139-373 <LEO>
A;Cross-references: EMBL:Z49205; NID:g798835; PIDN:CAA89066.1; PID:g798836
C;Comment: This receptor belongs to a family of G protein-coupled receptors. It responds to both ADP and ATP, and has several serine/threonine phosphorylation residues in the carboxyl terminus.
C;Genetics:
A;Gene: p2Y1; GDB:P2RY1
A;Cross-references: GDB:677125; OMIM:601167
A;Map position: 3pter-3qter
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F;52-77/Domain: transmembrane #status predicted <TM1>
F;88-111/Domain: transmembrane #status predicted <TM2>
F;124-152/Domain: transmembrane #status predicted <TM3>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;258,336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F;330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-dependent kinase) #status predicted

Query Match 28.7%; Score 474; DB 2; Length 373;
Best Local Similarity 37.3%; Pred. No. 4e-32;
Matches 107; Conservative 55; Mismatches 117; Indels 8; Gaps 6;

```
Qy         20 YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY 79
              ||| | | : || | |||   :: ::| || |:  :|||:|||:::|| :: ||| ||  |
Db         52 YYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYVLTLPALIFYY 111

Qy         80 ANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILI 138
               |     :|| :|   |:: | ||| |||||| ||  ||  : || :     ||: || |
Db        112 FNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLGRLKKKNAICI 171

Qy        139 SLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLS 197
              |: || :| : : |:| :  : | | :   | |  |        |||:| |:  | :||
Db        172 SVLVWLIVVVAISPILFYSGTGVRKNKTITCYDTTSDEYLRSYFIYSMCTTVAMFCVPLV 231

Qy        198 VMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIFSILFTPYHIMRNLRIASRL 256
              ::   |  :|  |  :    :  ||  |  ||:: : :|:: : |:|:|: : : :||
Db        232 LILGCYGLIVRALIYKDLDNS---PLRRKSIYLVIIVLTVFAVSYIPFHVMKTMNLRARL 288
```

```
Qy        257 D-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
              |   |  |     : : | :|| || ||| ::|| ||| || :|  |
Db        289 DFQTPAMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRRRL 335


RESULT 3
S33733
G protein-coupled receptor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C;Accession: S33733
R;Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.;
Burnstock, G.; Barnard, E.A.
FEBS Lett. 324, 219-225, 1993
A;Title: Cloning and functional expression of a brain G-protein-coupled ATP
receptor.
A;Reference number: S33733; MUID:93285340; PMID:8508924
A;Accession: S33733
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-362 <WEB>
A;Cross-references: EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:g395085
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match             28.6%;  Score 472.5;  DB 2;  Length 362;
  Best Local Similarity   35.9%;  Pred. No. 5.2e-32;
  Matches  110;  Conservative   58;  Mismatches  121;  Indels   17;  Gaps    8;

Qy         10 WLA----TEAILNK-----YYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFN 60
              | |    |:  | |     |||   | : || | |||   :: ::| |: |:  :||:||
Db         22 WAAGNATTKCSLTKTGFQFYYLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMFN 81

Qy         61 LSISDFAFLCTLPILIKSYANDKG-TYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLL 119
              |:::|| :: ||| ||  | |     :|||:|   |:: | ||| |||||| ||: ||
Db         82 LALADFLYVLTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYTG 141

Qy        120 MKYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINS-VPKEEGSNCIDYASSGNPE 178
              : :| :     ||: |: :|  |||||   : |:| :  : | : :   | |  :
Db        142 VVHPLKSLGRLKKKNAVYVSSLVWALVVAVIAPILFYSGTGVRRNKTITCYDTTADEYLR 201

Qy        179 HNLIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPL-DKPQRLVVLAVVIF 237
                 :||:| |:  | ||  |:   |  :|  |  :    :   ||  |   ||:: : :|
Db        202 SYFVYSMCTTVFMFCIPFIVILGCYGLIVKALIYKDLDNS---PLRRKSIYLVIIVLTVF 258

Qy        238 SILFTPYHIMRNLRIASRLD-SWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFYFLMGD 295
              :: : |:|:|: | : :|||   || |     : : | :|| || ||| ::|| ||| ||
Db        259 AVSYLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNSCVDPILYFLAGD 318

Qy        296 HYREML 301
               :|  |
Db        319 TFRRRL 324


RESULT 4
A47556
```

ATP receptor P2u - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C;Accession: A47556
R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.
A;Reference number: A47556; MUID:93281707; PMID:7685114
A;Accession: A47556
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373 <LUS>
A;Cross-references: GB:L14751; NID:g309457; PIDN:AAA39871.1; PID:g309458
C;Superfamily: ATP receptor P2u
C;Keywords: transmembrane protein

Query Match 22.6%; Score 373.5; DB 2; Length 373;
Best Local Similarity 33.5%; Pred. No. 9.8e-24;
Matches 94; Conservative 50; Mismatches 130; Indels 7; Gaps 5;

```
Qy         19 KY-YLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIK 77
              ||  |   | :  : ||  ||  :: :|  :| ||:|  |:|:|::||  :  :|||:|:
Db         32 KYVLLPVSYGVVCVLGLCLNVVALYIFLCRLKTWNASTTYMFHLAVSDSLYAASLPLLVY 91

Qy         78 SYA-NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAI 136
               ||  |   :  |||   |:: :|||| |||||| ||: | | :  |       :  :|
Db         92 YYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLHSLRWGRARYAR 151

Qy        137 LISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPL 196
              ::  || ||     |:| |: :  :     | | ::     | : ||  :  | | :|
Db        152 RVAAVVWVLVLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSSVMLGLLFAVPF 211

Qy        197 SVMCFFYYKMVVFLKRRSQQQATALPLDKPQ--RLVVLAVVIFSILFTPYHIMRNLRIAS 254
              ||:   |  |   | : :      ||  | :  | : | : :|:: | |:|: | |  :
Db        212 SVILVCYVLMARRLLKPAYGTTGGLPRAKRKSVRTIALVLAVFALCFLPFHVTRTLYYSF 271

Qy        255 RLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMG 294
              |  |    | |  ||   | :|||||  || ::|: |||
Db        272 R--SLDLSCHTLNAINMAYKITRPLASANSCLDPVLYFLAG 310
```

RESULT 5
JC4304
orphan G protein-coupled receptor - human
N;Alternate names: V28 protein
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 19-May-2000
C;Accession: JC4304
R;Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.
Gene 163, 295-299, 1995
A;Title: The orphan G-protein-coupled receptor-encoding gene V28 is closely related to genes for chemokine receptors and is expressed in lymphoid and neuraltissues.
A;Reference number: JC4304; MUID:96011651; PMID:7590284
A;Accession: JC4304
A;Molecule type: mRNA
A;Residues: 1-355 <RAP>

A;Cross-references: GB:U20350; NID:g665580; PIDN:AAA91783.1; PID:g665581
A;Experimental source: peripheral blood mononuclear cell
C;Comment: This protein is a cell-surface receptor which recognizes extracellular signals and transduces those signals into an intracellular response.
C;Comment: This protein is a key regulator of many immune and homeostatic responses, and interacts between the nervous and immune systems.
C;Genetics:
A;Gene: v28
A;Map position: 3pter-p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; lymphokine; transmembrane protein
F;35-57/Domain: transmembrane #status predicted <TM1>
F;66-88/Domain: transmembrane #status predicted <TM2>
F;104-125/Domain: transmembrane #status predicted <TM3>
F;146-165/Domain: transmembrane #status predicted <TM4>
F;197-217/Domain: transmembrane #status predicted <TM5>
F;230-254/Domain: transmembrane #status predicted <TM6>
F;275-296/Domain: transmembrane #status predicted <TM7>

Query Match 21.4%; Score 353; DB 2; Length 355;
Best Local Similarity 28.1%; Pred. No. 4.8e-22;
Matches 84; Conservative 66; Mismatches 133; Indels 16; Gaps 6;

```
Qy         16 ILNKYYLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPIL 75
              :    :|| ||:: |  ||:||: |||      |  : :::|| ||::||  |: |||
Db         28 VFGTVFLSIFYSVIFAIGLVGNLLVVFALTNSKKPKSVTDIYLLNLALSDLLFVATLPFW 87

Qy         76 IKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFA 135
                   |:|| : : :|           : || |:| ||:|||| :         :  :
Db         88 THYLINEKGLH-NAMCKFTTAFFFIGFFGSIFFITVISIDRYLAIVLAANSMNNRTVQHG 146

Qy        136 ILISLAVWALVTLEVLPMLTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLI 194
              : ||| |||   |   |   |     |:: : |: ||         :: ::    ||||:
Db        147 VTISLGVWAAAILVAAPQFMF----TKQKENECLGDYPEVLQEIWPVLRNVETNFLGFLL 202

Qy        195 PLSVMCFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIA 253
              || :| : |::::      :: ::| |:      :|::| |::| : :|||::|  |
Db        203 PLLIMSYCYFRIIQTLFSCKNHKKAKAI------KLILLVVIVFFLFWTPYNVMIFLETL 256

Qy        254 SRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
                | :|    :| ::   ::|  :|| :  :||: |   |: :|  |   :  | | |
Db        257 KLYDFFPSCDMRKDLRLALSVTETVAFSHCCLNPLIYAFAGEKFRRYL---YHLYGKCL 312
```

RESULT 6
S68679
G protein-coupled receptor - human
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S68679
R;Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.
FEBS Lett. 384, 260-264, 1996
A;Title: Molecular cloning and characterization of a novel orphan receptor (P(2P)) expressed in human pancreas that shows high structural homology to the P(2U) purinoceptor.
A;Reference number: S68679; MUID:96197801; PMID:8617367

A;Accession: S68679
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-365 <STA>
A;Cross-references: EMBL:X96597; NID:g1296631; PIDN:CAA65415.1; PID:g1296632
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor

Query Match 21.3%; Score 352; DB 2; Length 365;
Best Local Similarity 31.1%; Pred. No. 6e-22;
Matches 90; Conservative 59; Mismatches 122; Indels 18; Gaps 6;

```
Qy         22 LSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSY-A 80
              |   ||: |: ||  |   :: ::| :: |::: |:|:|::||  :: :|| ||  | |
Db         38 LPVSYAVVFVLGLGLNAPTLWLFIFRLRPWDATATYMFHLALSDTLYVLSLPTLIYYYAA 97

Qy         81 NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILISL 140
              ::   :|  :|   |:: : ||| |:|||| ||: ||| : :| |     :   | |: |
Db         98 HNHWPFGTEICKFVRFLFYWNLYCSVLFLTCISVHRYLGICHPLRALRWGRPRLAGLLCL 157

Qy        141 AVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVMC 200
              ||| :|   ::| | |: :  |     | |       :| : :|  :  | | :|  |
Db        158 AVWLVVAGCLVPNLFFVTTSNKGTTVLCHDTTRPEEFDHYVHFSSAVMGLLFGVPCLVTL 217

Qy        201 FFYYKMVVFLKRR-------SQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIA 253
                | |     ||       | | :: |   :  | : : : :|:: | |:|| | :
Db        218 VCYGLMA----RRLYQPLPGSAQSSSRL---RSLRTIAVVLTVFAVCFVPFHITRTIYYL 270

Qy        254 SRLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREML 301
              :||      |     :  :| :|||||  || ::|: | | || ||  |
Db        271 ARL--LEADCRVLNIVNVVYKVTRPLASANSCLDPVLYLLTGDKYRRQL 317
```

RESULT 7
A57160
chemokine (C-C) receptor 4 - human
N;Alternate names: C-C CKR-4
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: A57160
R;Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; Wells, T.N.C.
J. Biol. Chem. 270, 19495-19500, 1995
A;Title: Molecular cloning and functional expression of a novel CC chemokine receptor cDNA from a human basophilic cell line.
A;Reference number: A57160; MUID:95370289; PMID:7642634
A;Accession: A57160
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-360 <POW>
A;Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452
A;Note: source clone K5-5
C;Genetics:
A;Gene: GDB:CMKBR4
A;Cross-references: GDB:677463
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein;
transmembrane protein
F;40-65/Domain: transmembrane #status predicted <TM1>
F;76-97/Domain: transmembrane #status predicted <TM2>
F;112-133/Domain: transmembrane #status predicted <TM3>
F;151-175/Domain: transmembrane #status predicted <TM4>
F;208-226/Domain: transmembrane #status predicted <TM5>
F;243-264/Domain: transmembrane #status predicted <TM6>
F;291-308/Domain: transmembrane #status predicted <TM7>
F;29-276,110-187/Disulfide bonds: #status predicted
F;72,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status
predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
predicted
F;183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status
predicted

  Query Match 20.4%; Score 336.5; DB 2; Length 360;
  Best Local Similarity 29.4%; Pred. No. 1.2e-20;
  Matches 93; Conservative 60; Mismatches 132; Indels 31; Gaps 9;

```
Qy         14 EAILNKYYL--------------SAF--------YAIEFIFGLLGNVTVVFGYLFCMKNWN 52
              |:| : |||               ||        |:: |:||||||  ||   ||  |
Db         13 ESIYSNYYLYESIPKPCTKEGIKAFGELFLPPLYSLVFVFGLLGNSVVVL-VLFKYKRLR 71

Qy         53 S-SNVYLFNLSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTF 111
              | ::||| ||:|||  |: :||     || |:  :|  ||    ::     |: | |:
Db         72 SMTDVYLLNLAISDLLFVFSLPFW-GYYAADQWVFGLGLCKMISWMYLVGFYSGIFFVML 130

Qy        112 ISMDRYLLMKYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDY 171
              :|:|||| : :       :   : :: ||| |::     ||   |     :   : |
Db        131 MSIDRYLAIVHAVFSLRARTLTYGVITSLATWSVAVFASLPGFLFSTCYTERNHTYCKTK 190

Qy        172 ASSGNPEHNLIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVV 231
               |  :    :: || : :|| :||| :|  | | |::    |: |       :|  :::
Db        191 YSLNSTTWKVLSSLEINILGLVIPLGIM-LFCYSMII----RTLQHCKNEKKNKAVKMIF 245

Qy        232 LAVVIFSILFTPYHIMRNLRIASRLDSWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFY 290
              ||:|   :|||:|:  |     |:   | || :: :      |  |||::  :||| |
Db        246 AVVVLFLGFWTPYNIVLFLETLVELEVL-QDCTFERYLDYAIQATETLAFVHCCLNPIIY 304

Qy        291 FLMGDHYREMLISKFR 306
              | :|: :|: ::  |:
Db        305 FFLGEKFRKYILQLFK 320
```

RESULT 8
I55450
G protein-coupled P2 receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 19-May-2000
C;Accession: I55450
R;Chang, K.; Hanaoka, K.; Kumada, M.; Takuwa, Y.
J. Biol. Chem. 270, 26152-26158, 1995
A;Title: Molecular cloning and functional analysis of a novel P2 nucleotide
receptor.

A;Reference number: I55450; MUID:96064682; PMID:7592819
A;Accession: I55450
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <RES>
A;Cross-references: GB:D63665; NID:g1066007; PIDN:BAA09816.1; PID:g1066008
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor

Query Match 20.4%; Score 336; DB 2; Length 328;
Best Local Similarity 29.9%; Pred. No. 1.2e-20;
Matches 85; Conservative 52; Mismatches 137; Indels 10; Gaps 4;

```
Qy         22 LSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSYA- 80
              |   |::  : ||  || |:       :    | ||  ||:::|  : |:||:|| :||
Db         29 LPPVYSVVLVVGLPLNVCVIAQICASRRTLTRSAVYTLNLALADLLYACSLPLLIYNYAR 88

Qy         81 NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFRE-HFLQKKEFAILIS 139
               |   :||: |   |:: : ||: ||||| ||  ||| : :|    |    :  | ::
Db         89 GDHWPFGDLACRLVRFLFYANLHGSILFLTCISFQRYLGICHPLAPWHKRGGRRAAWVVC 148

Qy        140 LAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
              || :|| : ||   |  :  :   : | | :        | | : ||::|||:| : :
Db        149 GVVWLVVTAQCLPTAVFAATGIQRNRTVCYDLSPPILSTRYLPYGMALTVIGFLLPFTAL 208

Qy        200 CFFYYKMVVFLKRRSQQQATALPL-----DKPQRLVVLAVVIFSILFTPYHIMRNLRIAS 254
                | :|    :|  :|   | |:      |  |: |:   :| | | |:|| :   :|
Db        209 LACYCRMA---RRLCRQDGPAGPVAQERRSKAARMAVVVAAVFVISFLPFHITKTAYLAV 265

Qy        255 RLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYR 298
              |          :   : |  ||| |  || ::|| ::     :|
Db        266 RSTPGVSCPVLETFAAAYKGTRPFASANSVLDPILFYFTQQKFR 309
```

RESULT 9
A54946
P-2U nucleotide receptor - human
C;Species: Homo sapiens (man)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 17-Mar-1999
C;Accession: A54946
R;Parr, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J.C.; Erb, L.; Weisman, G.A.; Boucher, R.C.; Turner, J.T.
Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994
A;Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cystic fibrosis pharmacotherapy.
A;Reference number: A54946; MUID:94211846; PMID:8159738
A;Accession: A54946
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-375 <PAR>
A;Cross-references: GB:U07225
A;Note: parts of this sequence were confirmed by protein sequencing
C;Genetics:
A;Gene: GDB:P2RY2; HP2U; P2U
A;Cross-references: GDB:362713; OMIM:600041
A;Map position: 11q13.5-11q14.1
C;Superfamily: ATP receptor P2u

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 20.3%; Score 335.5; DB 2; Length 375;
Best Local Similarity 33.1%; Pred. No. 1.5e-20;
Matches 93; Conservative 52; Mismatches 127; Indels 9; Gaps 7;

```
Qy         19 KY-YLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIK 77
              ||  |   | :  : ||  |   :: :|  :| ||:|  |:|:|::||  :  :||:|:
Db         32 KYVLLPVSYGVVCVLGLCLNAVGLYIFLCRLKTWNASTTYMFHLAVSDALYAASLPLLVY 91

Qy         78 SYA-NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAI 136
               ||  |   :  |||   |:: :|||| |||||| ||: | | :  | |     :  :|
Db         92 YYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLRSLRWGRARYAR 151

Qy        137 LISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPL 196
              :: ||| ||     |:| |: :  :     | | ::       : ||  :  | | :|
Db        152 RVAGAVWVLVLACQAPVLYFVTTSARGP-LTCHDTSAPELFSRFVAYSSVMLGLLFAVPF 210

Qy        197 SVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVV--IFSILFTPYHIMRNLRIAS 254
              :|:   |  |   | : :   :  ||  | : :  :|||  :|:: | |:|: | |  :
Db        211 AVILVCYVLMARRLLKPAYGTSGGLPRAKRKSVRTIAVVLAVFALCFLPFHVTRTLYYSF 270

Qy        255 RLDSWPQGC-TQKAIKSIYTLTRPLAFLNSAINPIFYFLMG 294
              |  |    | |  ||   | :|| ||  || ::|: |||
Db        271 R--SLDLSCHTLNAINMAYKVTR-LASANSCLDPVLYFLAG 308
```

RESULT 10
I50241
G protein-coupled receptor 6H1 - chicken
N;Alternate names: purinoceptor 6H1
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Jun-2000
C;Accession: I50241; JC4618
R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A;Title: Identification of a G protein coupled receptor induced in activated T cells.
A;Reference number: I50241; MUID:93329058; PMID:8393036
A;Accession: I50241
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-308 <KAP>
A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384
R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A;Reference number: JC4618; MUID:96190677; PMID:8619790
A;Accession: JC4618
A;Molecule type: mRNA
A;Residues: 1-308 <WEB>
A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384
A;Experimental source: T-cells
C;Comment: This receptor plays a role in T-cell activation.
C;Genetics:
A;Gene: p2Y5
C;Superfamily: ATP receptor P2u

```
C;Keywords: G protein-coupled receptor; transmembrane protein
F;15-40/Domain: transmembrane #status predicted <TM1>
F;51-74/Domain: transmembrane #status predicted <TM2>
F;89-109/Domain: transmembrane #status predicted <TM3>
F;133-153/Domain: transmembrane #status predicted <TM4>
F;177-201/Domain: transmembrane #status predicted <TM5>
F;227-248/Domain: transmembrane #status predicted <TM6>
F;269-292/Domain: transmembrane #status predicted <TM7>

  Query Match             20.2%;  Score 333;  DB 2;  Length 308;
  Best Local Similarity   28.9%;  Pred. No. 1.9e-20;
  Matches   88;  Conservative   52;  Mismatches  123;  Indels   42;  Gaps    6;

Qy         19 KYYL-SAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIK 77
              || |    ::: |: ||: |   :: : | :|  | :  |: ||:|||  |: |||  |
Db         13 KYTLYGCVFSMVFVLGLIANCVAIYIFTFTLKVRNETTTYMLNLAISDLLFVFTLPFRIY 72

Qy         78 SYANDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAIL 137
               :      :|||||  :  : :||:| |||||| ||:||:| : :|||   |: |  | :
Db         73 YFVVRNWPFGDVLCKISVTLFYTNMYGSILFLTCISVDRFLAIVHPFRSKTLRTKRNARI 132

Qy        138 ISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLC----------- 186
              : :|||  |                 ||    :  | | ::|     |
Db        133 VCVAVWITVL----------------AGSTPASFFQSTNRQNNTEQRTCFENFPESTWKT 176

Qy        187 --------LTLLGFLIP--LSVMCFFYYKMVV-FLKRRSQQQATALPLDKPQRLVVLAVV 235
                     : ::|| ||  |:| |     ||:  | :        |   |  ::: : :|
Db        177 YLSRIVIFIEIVGFFIPLILNVTC---STMVLRTLNKPLTLSRNKLSKKKVLKMIFVHLV 233

Qy        236 IFSILFTPYHIMRNLRIASRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGD 295
              ||   | ||:|   |    |  :|       |::::| :|  :|  |   :|| |:   |
Db        234 IFCFCFVPYNITLILYSLMRTQTWINCSVVTAVRTMYPVTLCIAVSNCCFDPIVYYFTSD 293

Qy        296 HYREM 300
                 |:
Db        294 TNSEL 298


RESULT 11
I58186
probable G protein-coupled receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C;Accession: I58186
R;Harrison, J.K.; Barber, C.M.; Lynch, K.R.
Neurosci. Lett. 169, 85-89, 1994
A;Title: cDNA cloning of a G-protein-coupled receptor expressed in rat spinal
cord and brain related to chemokine receptors.
A;Reference number: I58186; MUID:94323113; PMID:8047298
A;Accession: I58186
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-354 <RES>
A;Cross-references: EMBL:U04808; NID:g2558635; PIDN:AAB87093.1; PID:g439861
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor
```

```
  Query Match             20.2%;  Score 332.5;  DB 2;  Length 354;
  Best Local Similarity   27.9%;  Pred. No. 2.5e-20;
  Matches   82;  Conservative   66;  Mismatches  125;  Indels   21;  Gaps    6;

Qy         21 YLSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSYA 80
              :|| ||:: | |||:||: ||       |: : :::|| ||::||  |: |||
Db         34 FLSIFYSLVFTFGLVGNLLVVLALTNSRKSKSITDIYLLNLALSDLLFVATLPFWTHYLI 93

Qy         81 NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILISL 140
              : :| : : :|           :  | |:| ||:|||| :         :  :  : |||
Db         94 SHEGLH-NAMCKLTTAFFFIGFFGGIFFITVISIDRYLAIVLAANSMNNRTVQHGVTISL 152

Qy        141 AVWALVTLEVLPMLTFINSVPKEEGSNCI-DYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
               |||   |   |   |     | : : |: ||         :: :  : :|||::|| :|
Db        153 GVWAAAILVASPQFMF----TKRKDNECLGDYPEVLQEIWPVLRNSEVNILGFVLPLLIM 208

Qy        200 CFFYYKMV-VFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIASRLDS 258
               | |:::|      :::::| |:      ||::| ||:| : :|||:|:  |      :
Db        209 SFCYFRIVRTLFSCKNRKKARAI------RLILLVVVVFFLFWTPYNIVIFLETLKFYNF 262

Qy        259 WPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYFKSL 312
              :|    :: ::   ::|  :|| :  :||  |   |:        |||:| : |
Db        263 FPSCGMKRDLRWALSVTETVAFSHCCLNPFIYAFAGE--------KFRRYLRHL 308
```

RESULT 12
JC4800
P2Y6 receptor - human
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 17-Nov-2000
C;Accession: JC4800; G02514
R;Communi, D.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 222, 303-308, 1996
A;Title: Cloning, functional expression and tissue distribution of the human P2Y6 receptor.
A;Reference number: JC4800; MUID:96222498; PMID:8670200
A;Accession: JC4800
A;Molecule type: mRNA
A;Residues: 1-328 <COM>
A;Cross-references: EMBL:X97058
A;Experimental source: placenta
R;Hammet, F.; Southey, M.C.; Somers, G.R.; Hutchins, A.M.; Venter, D.J.
submitted to the EMBL Data Library, March 1996
A;Reference number: H01373
A;Accession: G02514
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'M',4-328 <HAM>
A;Cross-references: EMBL:U52464; NID:g1407632; PIDN:AAB03572.1; PID:g1407633
C;Genetics:
A;Gene: P2Y6
C;Superfamily: ATP receptor P2u
C;Keywords: glycoprotein; placenta; receptor; transmembrane protein
F;26-52/Domain: transmembrane #status predicted <TMM1>
F;63-86/Domain: transmembrane #status predicted <TMM2>
F;104-122/Domain: transmembrane #status predicted <TMM3>
F;143-167/Domain: transmembrane #status predicted <TMM4>
```
```

```
F;193-216/Domain: transmembrane #status predicted <TMM5>
F;241-264/Domain: transmembrane #status predicted <TMM6>
F;283-305/Domain: transmembrane #status predicted <TMM7>
F;5,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             20.1%;  Score 332;  DB 2;  Length 328;
  Best Local Similarity   30.6%;  Pred. No. 2.5e-20;
  Matches   90;  Conservative   48;  Mismatches  136;  Indels   20;  Gaps    6;

Qy         22 LSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSYA- 80
              |   |:     ||  |: |:       :    : ||  ||:::|  : |:|||:|| :||
Db         29 LPPVYSAVLAAGLPLNICVITQICTSRRALTRTAVYTLNLALADLLYACSLPLLIYNYAQ 88

Qy         81 NDKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFRE-HFLQKKEFAILIS 139
               |   :||  |   |:: : ||: ||||||  ||  ||| : :|    |    :  | |:
Db         89 GDHWPFGDFACRLVRFLFYANLHGSILFLTCISFQRYLGICHPLAPWHKRGGRRAAWLVC 148

Qy        140 LAVWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVM 199
              :|||  || : ||   |  :  :   : | | :      | : | : ||::|||:| : :
Db        149 VAVWLAVTTQCLPTAIFAATGIQRNRTVCYDLSPPALATHYMPYGMALTVIGFLLPFAAL 208

Qy        200 CFFYYKMVVFLKRRSQQQATALPL-----DKPQRLVVLAVVIFSILFTPYHIMRNLRIAS 254
                |  :     |  :|   | |:      |  |: |:    |:| | |:|| :   :|
Db        209 LACYCLLAC---RLCRQDGPAEPVAQERRGKAARMAVVVAAAFAISFLPFHITKTAYLAV 265

Qy        255 RLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPI-FYFLMGDHYREMLISKFRQ 307
              |          :|  : |  ||| |  || ::|| |||            |||:
Db        266 RSTPGVPCTVLEAFAAAYKGTRPFASANSVLDPILFYFTQ---------KKFRR 310


RESULT 13
A45177
chemokine (C-C) receptor 1 - human
N;Alternate names: C-C CKR-1; macrophage inflammatory protein-1-alpha receptor
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C;Accession: A45177; I55671
R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.
Cell 72, 415-425, 1993
A;Title: Molecular cloning, functional expression, and signaling characteristics
of a C-C chemokine receptor.
A;Reference number: A45177; MUID:93161416; PMID:7679328
A;Accession: A45177
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-355 <NEO>
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
A;Experimental source: HL60 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)
R;Gao, J.
J. Exp. Med. 177, 1421-1427, 1993
A;Title: Structure and functional expression of the human macrophage
inflammatory 1 alpha (MIP-1alpha)/RANTES receptor.
A;Reference number: I55671; MUID:93240122; PMID:7683036
A;Accession: I55671
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
```

A;Residues: 1-355 <RES>
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417
C;Genetics:
A;Gene: GDB:CMKBR1; CMKR-1
A;Cross-references: GDB:138446; OMIM:601159
A;Map position: 3p21-3p21
C;Superfamily: vertebrate rhodopsin
C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein;
phosphoprotein; transmembrane protein
F;36-60/Domain: transmembrane #status predicted <TM1>
F;71-91/Domain: transmembrane #status predicted <TM2>
F;108-129/Domain: transmembrane #status predicted <TM3>
F;147-171/Domain: transmembrane #status predicted <TM4>
F;205-223/Domain: transmembrane #status predicted <TM5>
F;240-264/Domain: transmembrane #status predicted <TM6>
F;288-305/Domain: transmembrane #status predicted <TM7>
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;24-273,106-183/Disulfide bonds: #status predicted
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status
predicted

  Query Match 19.9%; Score 328; DB 2; Length 355;
  Best Local Similarity 29.0%; Pred. No. 5.9e-20;
  Matches 85; Conservative 63; Mismatches 127; Indels 18; Gaps 8;

```
Qy         22 LSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSYAN 81
              |   |:: |: ||:||: ||   :   :  | :::|| ||:|||  || |||  |
Db         37 LPPLYSLVFVIGLVGNILVVLVLVQYKRLKNMTSIYLLNLAISDLLFLFTLPFWIDYKLK 96

Qy         82 DKGTYGDVLC--ISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILIS 139
              |   :|| :|  :|  |  :| ||: | |:  :::|||| : :       :   | :: |
Db         97 DDWVFGDAMCKILSGFY--YTGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITS 154

Qy        140 LAVWALVTLEVLPMLTFINSVPKEEGSNC-IDYASSGNPEHNLIYSLCLTLLGFLIPLSV 198
              : :|||  |  :| | |  :  :     | : :      |  |  :| | | | ::|| |
Db        155 IIIWALAILASMPGLYFSKTQWEFTHHTCSLHFPHESLREWKLFQALKLNLFGLVLPLLV 214

Qy        199 MCFFYYKMVVFLKRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNLRIASRLD- 257
              |   |  ::  | ||  :: :     |  ||: : ::|| : :|||::   : |:   |
Db        215 MIICYTGIIKILLRRPNEKKS-----KAVRLIFVIMIIFFLFWTPYNL--TILISVFQDF 267

Qy        258 SWPQGCTQ-KAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYREMLISKFRQYF 309
               :   | | : :     :|  :|: :  :||: |  :|: :|: |    || |
Db        268 LFTHECEQSRHLDLAVQVTEVIAYTHCCVNPVIYAFVGERFRKYL----RQLF 316
```

RESULT 14
JC4587
chemokine (C-C) receptor 4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 20-Jun-2000
C;Accession: JC4587
R;Hoogewerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.
Biochem. Biophys. Res. Commun. 218, 337-343, 1996
A;Title: Molecular cloning of murine CC CKR-4 and high affinity binding of
chemokines to murine and human CC CKR-4.
A;Reference number: JC4587; MUID:96136324; PMID:8573157

A;Accession: JC4587
A;Molecule type: mRNA
A;Residues: 1-360 <HOO>
A;Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852
A;Experimental source: thymus
C;Genetics:
A;Gene: cc ckr-4
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; phosphoprotein; receptor; thymus
F;2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;72,202,350/Binding site: phosphate (Ser) (covalent) (by casein kinase II)
#status predicted
F;145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
predicted
F;321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status
predicted

  Query Match 19.8%; Score 326.5; DB 2; Length 360;
  Best Local Similarity 28.4%; Pred. No. 8e-20;
  Matches 93; Conservative 57; Mismatches 136; Indels 41; Gaps 10;

```
Qy         14 EAILNKYY----------------------LSAFYAIEFIFGLLGNVTVVFGYLFCMKNWN 52
              | : | ||                      |   |:: |: || ||  ||   ||  |
Db         13 ETVYNSYYFYESMPKPCTKEGIKAFGEVFLPPLYSLVFLLGLFGNSVVVL-VLFKYKRLK 71

Qy         53 S-SNVYLFNLSISDFAFLCTLPILIKSYANDKGTYGDVLCISNRYVLHTNLYTSILFLTF 111
              | ::||| ||:|||  |: :||     || |:  :|  ||    ::     |: | |:
Db         72 SMTDVYLLNLAISDLLFVLSLPFW-GYYAADQWVFGLGLCKIVSWMYLVGFYSGIFFIML 130

Qy        112 ISMDRYLLMKYPFREHFLQKKEFAILISLAVWALVTLEVLPMLTFINSVPKEEGSNCIDY 171
              :|:|||| : :       :   : :: ||  |::     || | |     :   : |
Db        131 MSIDRYLAIVHAVFSLKARTLTYGVITSLITWSVAVFASLPGLLFSTCYTEHNHTYCKTQ 190

Qy        172 ASSGNPEHNLIYSLCLTLLGFLIPLSVMCFFYYKMVVFLKRRSQQQATALPLDKPQRLVV 231
               |  :    :: || : :|| |||| :|  |:| |::    |: |       ::  |::
Db        191 YSVNSTTWKVLSSLEINVLGLLIPLGIM-LFWYSMII----RTLQHCKNEKKNRAVRMIF 245

Qy        232 LAVVIFSILFTPYHIMRNLRIASRLDSWPQGCT-QKAIKSIYTLTRPLAFLNSAINPIFY 290
              ||:|   :|||::: |     |:   | || :: :      |  | |::  :||: |
Db        246 GVVVLFLGFWTPYNVVLFLETLVELEVL-QDCTLERYLDYAIQATETLGFIHCCLNPVIY 304

Qy        291 FLMGDHYREMLISKFRQYFKSLTSFRT 317
              | :|:        |||:|   |  |||
Db        305 FFLGE--------KFRKYITQL--FRT 321
```

RESULT 15
JN0605
somatostatin receptor 4 - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C;Accession: JN0605; JN0762; A47457
R;Xu, Y.; Song, J.; Bruno, J.F.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 193, 648-652, 1993
A;Title: Molecular cloning and sequencing of a human somatostatin receptor,
hSSTR4.
A;Reference number: JN0605; MUID:93290656; PMID:8512564

A;Accession: JN0605
A;Molecule type: DNA
A;Residues: 1-388 <XUY>
A;Cross-references: GB:L14856; NID:g292499; PIDN:AAA36623.1; PID:g292500
R;Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.;
Ihara, Y.; Li, Q.; Imura, H.; Seino, S.; Seino, Y.
Biochem. Biophys. Res. Commun. 195, 844-852, 1993
A;Title: Cloning, functional expression and pharmacological characterization of
a fourth (hSSTR4) and a fifth (hSSTR5) human somatostatin receptor subtype.
A;Reference number: JN0762; MUID:93384611; PMID:8373420
A;Accession: JN0762
A;Molecule type: DNA
A;Residues: 1-388 <YAM>
A;Cross-references: GB:D16826; NID:g693907; PIDN:BAA04106.1; PID:g693908
R;Rohrer, L.; Raulf, F.; Bruns, C.; Buettner, R.; Hofstaedter, F.; Schule, R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4196-4200, 1993
A;Title: Cloning and characterization of a fourth human somatostatin receptor.
A;Reference number: A47457; MUID:93248256; PMID:8483934
A;Accession: A47457
A;Molecule type: DNA
A;Residues: 1-82,'T',84-364,'K',366-388 <ROH>
A;Cross-references: GB:L07833; NID:g307429; PIDN:AAA60565.1; PID:g307430
A;Note: sequence extracted from NCBI backbone (NCBIN:130856, NCBIP:130858)
C;Comment: This protein mediates the diverse actions of the tetradecaptide
somatostatin.
C;Genetics:
A;Gene: GDB:SSTR4
A;Cross-references: GDB:202662; OMIM:182454
A;Map position: 20p11.2-20p11.2
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor;
lipoprotein; phosphoprotein; thiolester bond; transmembrane protein
F;47-73/Domain: transmembrane #status predicted <TM1>
F;84-109/Domain: transmembrane #status predicted <TM2>
F;121-142/Domain: transmembrane #status predicted <TM3>
F;162-184/Domain: transmembrane #status predicted <TM4>
F;208-238/Domain: transmembrane #status predicted <TM5>
F;257-284/Domain: transmembrane #status predicted <TM6>
F;291-314/Domain: transmembrane #status predicted <TM7>
F;24/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;119-198/Disulfide bonds: #status predicted
F;161,253/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase)
#status predicted
F;327/Binding site: palmitate (Cys) (covalent) #status predicted

  Query Match 19.7%; Score 325.5; DB 2; Length 388;
  Best Local Similarity 28.4%; Pred. No. 1e-19;
  Matches 82; Conservative 66; Mismatches 110; Indels 31; Gaps 5;

```
Qy         22 LSAFYAIEFIFGLLGNVTVVFGYLFCMKNWNSSNVYLFNLSISDFAFLCTLPILIKSYAN 81
              :   ||:  : ||:||  |:|  |   |   ::|:|| ||:::|  |: ::| :  | |
Db         50 IQCIYALVCLVGLVGNALVIFVILRYAKMKTATNIYLLNLAVADELFMLSVPFVASSAAL 109

Qy         82 DKGTYGDVLCISNRYVLHTNLYTSILFLTFISMDRYLLMKYPFREHFLQKKEFAILISLA 141
                 :| ||| :   |   |::||:  || :|:|||: : :| |    ::   | ||:|
Db        110 RHWPFGSVLCRAVLSVDGLNMFTSVFCLTVLSVDRYVAVVHPLRAATYRRPSVAKLINLG 169
```

```
Qy        142 VWALVTLEVLPMLTFINSVPKEEGSNCIDYASSGNPEHNLIYSLCLTLLGFLIPLSVMCF 201
              ||    |  ||:  | :: |   |          :|  : :: :   |||||:|:  :
Db        170 VWLASLLVTLPIAIFADTRPARGGQAVACNLQWPHPAWSAVFVVYTFLLGFLLPVLAIGL 229

Qy        202 FYYKMV-----VFL------KRRSQQQATALPLDKPQRLVVLAVVIFSILFTPYHIMRNL 250
               |  :|     | |      :|||::: |        |||:: ||:| : : |:::::  |
Db        230 CYLLIVGKMRAVALRAGWQQRRRSEKKIT--------RLVLMVVVVFVLCWMPFYVVQLL 281

Qy        251 R-IASRLDSWPQGCTQKAIKSIYTLTRPLAFLNSAINPIFYFLMGDHYR 298
              : : ||:           ::  ::  |:: ||  ||| |  : |::|
Db        282 NLVVTSLDA----------TVNHVSLILSYANSCANPILYGFLSDNFR 319
```

Search completed: December 12, 2003, 18:09:05
Job time : 21 secs